

score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

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Description
T08277 Sequence 2
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L23788 Bos taurus
I12266 Sequence 1
M12621 Bovine lyso
I09315 Sequence 1
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M26246 Bovine lyso
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M26244 Bovine lyso
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M32445 Sheep lysoz
M32442 Sheep lysoz
M32447 Sheep lysoz
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M32459 A. axis, lyso
M32500 A. axis, lyso
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M26240 Bovine lyso
L23757 Bos taurus
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U76918 Trachypithe
X60235 P. entellus
U76916 Colobus que
I19380 Bos taurus
X60238 M. mulatta m
U76920 Cercopithec
U76919 Papio hamad
X60237 C. aethiops
U76914 Pongo pygma
U76912 Pan troglodyd
M23113 Human lysoz
X03801 Human lysoz
E01888 DNA sequen
E02193 DNA encodin
BC004447 Homo sapi
U76921 Samitri sci
U76913 Gorilla sci
K231738 Sequence
M23119 Human lysoz
U76923 Callitrich
U76922 Saguinus oer
U25677 Homo sapien





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 QY 126 CCTGCAAACTGTTGTGTGTTGACCAATGGAAGCAAGTATTAACCAAAAGCTCAAA 185  
 Db 121 CCTGCAAACTGTTGTGTGTTGACCAATGGAAGCAAGTATTAACCAAAAGCTCAAA 180  
 QY 186 CTACATCTCAGCAGTGAAGCACTGATTAATGGAATATTCAGATCAACCAAAAGTGTG 245  
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 Db 301 AATGAAATGACATGCTAAGCTGAGCGTGTGCAAAACATATGTCAGTACGCAAG 360  
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 DEFINITION Sequence 1 from Patent WO 8904320.  
 ACCESSION 109315  
 VERSION 109315.1 GI:587976  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 963)  
 AUTHORS Digan,M.E., Harpold,M.M., Lair,S.V., Thill,G.P., Siegel,R.S., Ellis,S.B. and Williams,M.E.  
 TITLE PRODUCTION OF ANIMAL LYSOZYME c VIA SECRETION FROM PICHA PASTORIS AND COMPOSITION THEREFOR  
 JOURNAL Patent: WO 8904320-A 1 18-MAY-1989;  
 FEATURES  
 source location/Qualifiers  
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 Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 366 CATTACAGCTGGGTGCGATGAGAAAGTCAATGTCGAGACCATGACGTGACGTTACGT 425  
 Db 384 CATTACAGCTGGGTGCGATGAGAAAGTCAATGTCGAGACCATGACGTGACGTTACGT 443  
 QY 426 TGAGGTTGCACCTGTAA 444  
 Db 444 TGAGGTTGCACCTGTAA 462  
 RESULT 7  
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 DEFINITION Bovine lysozyme c isozyne 3a mRNA, complete cds.  
 ACCESSION M26242 J04831 M27180  
 VERSION M26242.1 GI:163322  
 KEYWORDS  
 SOURCE Lysozyme.  
 ORGANISM Bovine abomasum, cDNA to mRNA, clone lambda-cbl[26,28].  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 1082)  
 AUTHORS Irwin,D.M. and Wilson,A.C.  
 TITLE Multiple cDNA sequences and the evolution of bovine stomach lysozyme  
 JOURNAL J. Biol. Chem. 264 (19), 11387-11393 (1989)  
 MEDLINE 89291894  
 PUBMED 2738070  
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 23-JUN-1989  
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 Matches 433; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY	301	GAATTATGCAAAATGACATCGCTTAAAGCTGTACAGTGTGCAAAGCATATTGTCAAGTAG	360
Db	309	GAATTATGCAAAATGACATCGCCAAAGCGGTACCATGTGTCAAAGCATATTGTCAAGTAG	368
QY	361	CAGGCATTACAGCCTCGGTGGTGCAATGTGAAAAAGTATTGTGCAAGCATGACGTACAGT	420
Db	369	CAGGCATTACAGCATGGGTGGCAATGTGAAAAAGTACTGTGCAAGCATGACGTACAGT	428
QY	421	TACGTTGAGGTTGCACCCCTGTAA	444
Db	429	TATGTTCAAGGTTGCACCCCTGTAA	452

RESULT 8	BOVIS21B						
LOCUS	BOVIS21B	891 bp	1	1	1	1	1
DEFINITION	Bovine lysozyme c isozyme 1b mRNA, complete cds.						
ACCESSION	M26246 J04831 M27179						
VERSION	M26246.1 GI:163312						
KEYWORDS	lysozyme.						
SOURCE	Bovine abomasum, cDNA to mRNA, clones lambda-CBL[3,4,35].						
ORGANISM	Bos taurus						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.						
REFERENCE	1 (bases 1 to 891)						
AUTHORS	Irwin,D.M. and Wilson,A.C.						
TITLE	Multiple cDNA sequences and the evolution of bovine stomach lysozyme						
JOURNAL	J. Biol. Chem. 264 (19), 11387-11393 (1989)						
MEDLINE	89291894						
PUBMED	2738070						
COMMENT	Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 23-JUN-1989.						

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	8. .61
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Db	8	ATGAAGGCTCATATTCTGGGGTTTCTCTCTTCTGCGCTGTCGAAGCAAGCTC	67	
QY	61	TTTGAGAGATGTGACCTTGCCAGAACTGTGAAGAACTTGACACTGACGCTATTAAAGGA	120	
Db	68	TTTGAGAGATGTGACCTTGCCAGAACTGTGAAGAACTTGACACTGAGAGCTATTAAAGGA	127	
QY	121	GTACACCTGGCAAACTGGTGTGCTTTGACCAAAATGGGAAGCAAGTTATTAAACAAAACCT	180	
Db	128	GTACATCTGGCAAACTGGCTGTGTTTGACCAAAATGGGAAGCAAGTTATTAAACAAAACCT	187	

QY	181	ACAACTACAACTCAGCAGTGAAGCAGCTATTATGGATATTTCAGATCAACAGCAAA	240
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QY	241	TGCTGTGTATATGATGGCAAAACCCCTATATGCACTTGACGGCTCTCATATATCCTCAGC	300
Db	248	TGCTGTGTATATGATGGCAAAACCCCAACAGCTTGACGGCTCTCATATATCCTCAGC	307
QY	301	GAATTATATGAAAAATACATCGCTTAACCTGTAGCGGTGCAAGACATATTGTACAGTAG	360
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QY	361	CAAGCATTTACAGCCTGGGTGGCATGAAAAATCATTTGTGAGACCATGACGTCCAGCT	420
Db	368	CAAGCATTTACAGCATGGGTGGCATGAAAAATCATCTGTGAGACCATGACGTCCAGCT	427
QY	421	TACGTTGAGGGTTGCACCCCTTTAA	444
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Db	23	ATGAAGGCTCTCATTAATTCGTGGGGTTTCTTCTTCTTGTGCTGTCCAGGCAAGCTC	82	
QY	61	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGAGCGGCTATTAAGGA	120	
Db	83	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGAGATGGCTATTAAGGA	142	

QY 121 GTCAGCTGGCAAACTGTTGTGTGGACCAAAATGGGAAGCAGTATATAACACAAAAGCT 180  
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RESULT 10  
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 LOCUS  
 DEFINITION Bovine lysozyme c lysozyme 2c mRNA, complete cds.  
 ACCESSION M26244 J04831 M27183  
 VERSION M26244.1 GI:163318  
 KEYWORDS  
 SOURCE Lysozyme.  
 ORGANISM Bos taurus  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 877)  
 Irwin,D.M. and Wilson,A.C.  
 Multiple cDNA sequences and the evolution of bovine stomach  
 lysozyme  
 J. Biol. Chem. 264 (19), 11387-11393 (1989)  
 MEDLINE 89291894  
 PUBMED 2738070

REFERENCE  
 AUTHORS Irwin,D.M. and Wilson,A.C.  
 TITLE Multiple cDNA sequences and the evolution of bovine stomach  
 lysozyme  
 J. Biol. Chem. 264 (19), 11387-11393 (1989)  
 MEDLINE 89291894  
 PUBMED 2738070  
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
 by D.M.Irwin, 23-JUN-1989.

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 Matches 398; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 106 GACGGCTATAGGAGATGACCTGGCAAACTGTTGTGTGGACCAAAATGGGAAGCAGT 165  
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RESULT 11  
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 LOCUS  
 DEFINITION Sheep lysozyme 3a (lyz3a) mRNA, complete cds.  
 ACCESSION M32486 J05279  
 VERSION M32486.1 GI:165971  
 KEYWORDS  
 SOURCE Lysozyme 3a.  
 ORGANISM Sheep abomasum, CDNA to mRNA.  
 Ovis aries  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Caprinae; Ovis.  
 1 (bases 1 to 875)  
 Irwin,D.M. and Wilson,A.C.  
 Concerted evolution of ruminant stomach lysozymes. Characterization  
 of lysozyme cDNA clones from sheep and deer  
 J. Biol. Chem. 265 (9), 4944-4952 (1990)  
 MEDLINE 90202968  
 PUBMED 2318875

REFERENCE  
 AUTHORS Irwin,D.M. and Wilson,A.C.  
 TITLE Concerted evolution of ruminant stomach lysozymes. Characterization  
 of lysozyme cDNA clones from sheep and deer  
 J. Biol. Chem. 265 (9), 4944-4952 (1990)  
 MEDLINE 90202968  
 PUBMED 2318875  
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
 by D.M.Irwin, 01-MAR-1990.

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Query Match 82.8%; Score 367.6; DB 4; Length 875;  
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 Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 115 AAGGAGTCAGCCCTGGCAAACTGTTGTGTTGGACCAATGGGAAGCATTATACACA 174  
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Db 241 TGCAGCGAATTAATGAAATATGACATGCTAAAGCTGTAGCGGTGTGCAAGCATATTGTC 300  
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Db 361 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 390

## RESULT 12

LOCUS SHPLZM1B 881 bp mRNA linear MAM 27-Apr-1993  
DEFINITION Sheep lysozyme 1b (12mb) mRNA, 3' end.  
ACCESSION M32493 J05279  
VERSION M32493.1 GI:165965  
KEYWORDS lysozyme 1b.  
SOURCE Sheep abomasum, CDNA to mRNA.  
ORGANISM Ovis aries

REFERENCE  
AUTHORS Irwin,D.M. and Wilson,A.C.  
TITLE 1 (bases 1 to 881)  
JOURNAL Concerted evolution of ruminant stomach lysozymes. Characterization  
MEDLINE of lysozyme cDNA clones from sheep and deer  
PUBMED J. Biol. Chem. 265 (9), 4944-4952 (1990)  
90202968  
2318875

COMMENT  
Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M.Irwin, 01-MAR-1990.

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OGITAMVAMKSHCRDHVSVYEGCSL"

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misc\_feature 1..17  
/note="PCR primer"  
BASE COUNT 285 a 145 c 182 g 269 t  
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Query Match 82.8%; Score 367.6; DB 4; Length 881;  
Best Local Similarity 96.4%; Pred. No. 1.6e-90;  
Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGCGGCTAT 114  
|||||  
Db 1 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGCGGCTAT 60

QY 115 AAGGAGTCAGCCCTGGCAAACTGTTGTGTTGGACCAATGGGAAGCATTATACACA 174  
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Db 61 AAGGAGTCAGCCCTGGCAAACTGTTGTGTTGGACCAATGGGAAGCATTATACACA 120  
QY 175 AAAGCTACAACTACAACTCTAGCAGTGAAGCAGCTATTTATGGATTTTCAGATCAC 234  
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Db 121 AAAGCTACAACTACAACTCTAGCAGTGAAGCAGCTATTTATGGATTTTCAGATCAC 180  
QY 235 AGCAATAGTGTGTATGATGATGCAAAACCCCTAATGATGATGATGATGATGATGATG 294  
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Db 181 AGCAATAGTGTGTATGATGATGCAAAACCCCTAATGATGATGATGATGATGATGATG 240  
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Db 241 TGCAGCGAATTAATGAAATATGACATGCTAAAGCTGTAGCGGTGTGCAAGCATATTGTC 300  
QY 355 AGTGAAGCAAGCATTACAGCCTGGGTGGCATGGAAGATCATTTGTGAGACCATGACGTC 414  
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Db 301 AGTGAAGCAAGCATTACAGCCTGGGTGGCATGGAAGATCATTTGTGAGACCATGACGTC 360  
QY 415 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 444  
|||||  
Db 361 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 390

## RESULT 13

LOCUS SHPLZM1C 881 bp mRNA linear MAM 27-Apr-1993  
DEFINITION Sheep lysozyme 1c (121c) mRNA, 3' end.  
ACCESSION M32494 J05279  
VERSION M32494.1 GI:165967  
KEYWORDS lysozyme 1c.  
SOURCE Sheep abomasum, CDNA to mRNA.  
ORGANISM Ovis aries

REFERENCE  
AUTHORS Irwin,D.M. and Wilson,A.C.  
TITLE 1 (bases 1 to 881)  
JOURNAL Concerted evolution of ruminant stomach lysozymes. Characterization  
MEDLINE of lysozyme cDNA clones from sheep and deer  
PUBMED J. Biol. Chem. 265 (9), 4944-4952 (1990)  
90202968  
2318875

COMMENT  
Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M.Irwin, 01-MAR-1990.

FEATURES  
source location/Qualifiers  
1..881  
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/db\_xref="taxon:9940"  
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1..390  
/note="lysozyme 1c precursor"  
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OGITAMVAMKSHCRDHVSVYEGCSL"

mat\_peptide 1..387  
/product="lysozyme 1c"  
misc\_feature 1..17  
/note="PCR primer"  
BASE COUNT 285 a 144 c 183 g 269 t  
ORIGIN

Query Match 82.8%; Score 367.6; DB 4; Length 881;  
Best Local Similarity 96.4%; Pred. No. 1.6e-90;  
Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGCGGCTAT 114  
|||||  
Db 1 AAGGCTTTGAGAGATGAGCTTGCAGAACTCGAAGAACTGGAGCGGCTAT 60

QY 115 AAGGAGTCAGCCTGGCAAACTGGTGTGTTTGACCAAAATGGCAAGCACTTATACACA 174  
|||||  
Db 61 AAGGAGTCAGCCTGGCAAACTGGTGTGTTTGACCAAAATGGCAAGCACTTATACACA 120  
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QY 175 AAGGCTACAACTACATCTAGCAGTGAAGCAGTATGAGATTTTGCATCAGC 234  
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QY 235 AGCAATGTGTGTATATGATGAGCAAAACCCCTAATGAGTGAAGGCTGTCATGATCC 294  
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Db 181 AGCAATGTGTGTATATGATGAGCAAAACCCCTAATGAGTGAAGGCTGTCATGATCC 240  
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QY 295 TGCAGCGAATTAATGGAATAATGACATGCTAAAGCTGAGCGTGTGCAAGCATATGTC 354  
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Db 241 TGCAGCGAATTAATGGAATAATGACATGCTAAAGCTGAGCGTGTGCAAGCATATGTC 300  
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QY 355 AGTGAAGCAAGCATTAACGCTGGTGGCATGGAAGAGTATGATGAGACCATGAGCTC 414  
|||||  
Db 301 AGTGAAGCAAGCATTAACGCTGGTGGCATGGAAGAGTATGATGAGACCATGAGCTC 360  
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QY 415 AGCAGTTACGTTGAGGCTTGCACCTGTAA 444  
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Db 361 AGCAGTTACGTTGAGGCTTGCACCTGTAA 390  
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RESULT 14  
SHP12M2A 881 bp mRNA linear MAM 27-APR-1993  
LOCUS SHP12M2A  
DEFINITION Sheep lysozyme 2a (lyz2a) mRNA, 3' end.  
ACCESSION M32495.1  
VERSION M32495.1 GI:165969  
KEYWORDS lysozyme 2a.  
SOURCE Sheep abomasum, cDNA to mRNA.  
ORGANISM Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
1 (bases 1 to 881)  
Irwin, D.M. and Wilson, A.C.  
Concerted evolution of ruminant stomach lysozymes. Characterization  
of lysozyme cDNA clones from sheep and deer  
J. Biol. Chem. 265 (9), 4944-4952 (1990)  
90202968  
PUBMED 2318875  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M.Irwin, 01-MAR-1990.  
FEATURES  
source location/Qualifiers  
1..881  
/organism="Ovis aries"  
/db\_xref="taxon:9940"  
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1..390  
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mat\_peptide 1..387  
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misc\_feature 1..17  
/note="PCR primer"  
BASE COUNT 287 a 144 c 183 g 267 t  
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Query Match 82.8%; Score 367.6; DB 4; Length 881;  
Best Local Similarity 96.4%; Pred. No. 1.6e-90;  
Matches 376; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 114  
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Db 1 AAGGCTTTGAGAGATGAGCTTGCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 60  
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QY 115 AAGGAGTCAGCCTGGCAAACTGGTGTGTTTGACCAAAATGGCAAGCACTTATACACA 174  
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Db 61 AAGGAGTCAGCCTGGCAAACTGGTGTGTTTGACCAAAATGGCAAGCACTTATACACA 120  
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QY 175 AAGGCTACAACTACATCTAGCAGTGAAGCAGTATGAGATTTTGCATCAGC 234  
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Db 241 TGCAGCGAATTAATGGAATAATGACATGCTAAAGCTGAGCGTGTGCAAGCATATGTC 300  
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QY 355 AGTGAAGCAAGCATTAACGCTGGTGGCATGGAAGAGTATGATGAGACCATGAGCTC 414  
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Db 301 AGTGAAGCAAGCATTAACGCTGGTGGCATGGAAGAGTATGATGAGACCATGAGCTC 360  
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QY 415 AGCAGTTACGTTGAGGCTTGCACCTGTAA 444  
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Db 361 AGCAGTTACGTTGAGGCTTGCACCTGTAA 390  
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RESULT 15  
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LOCUS SHP12M1A  
DEFINITION Sheep lysozyme 1a (lyz1a) mRNA, 3' end.  
ACCESSION M32492.1  
VERSION M32492.1 GI:165963  
KEYWORDS lysozyme 1a.  
SOURCE Sheep abomasum, cDNA to mRNA.  
ORGANISM Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
1 (bases 1 to 881)  
Irwin, D.M. and Wilson, A.C.  
Concerted evolution of ruminant stomach lysozymes. Characterization  
of lysozyme cDNA clones from sheep and deer  
J. Biol. Chem. 265 (9), 4944-4952 (1990)  
90202968  
PUBMED 2318875  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M.Irwin, 01-MAR-1990.  
FEATURES  
source location/Qualifiers  
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CDS  
1..390  
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misc\_feature 1..15  
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Best Local Similarity 96.2%; Pred. No. 4.5e-90;  
Matches 373; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 55 AAGGCTTTGAGAGATGAGCTTGCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 114  
|||||  
Db 1 AAGGCTTTGAGAGATGAGCTTGCAGAACTGTGAAGAACTTGAGTGAAGCGCTAT 60  
|||||

```
QY 115 AAGGAGTCAGCCTGGCAAACTGGTGTGTTGACCAATGGGAAAAGCAGTTATAACACA 174
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Db 61 AAGGAGTCAGCCTGGCAAACTGGTGTGTTGACCAATGGGAAAAGCAGTTATAACACA 120
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QY 175 AAAGCTACAACTACAACTCCTAGACAGTGAAGCACTGATTATGGATATTTGAGATCAAC 234
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Db 121 AAAGCTACAACTACAACTCCTAGACAGTGAAGCACTGATTATGGATATTTGAGATCAAC 180
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QY 235 AGCAATGGTGGTATATGATGACAAAACCCCTAATGCAGTTGACGGCTGTATGATCC 294
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Db 181 AGCAATGGTGGTATATGATGACAAAACCCCTAATGCAGTTGACGGCTGTATGATCC 240
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QY 295 TGCAGCGAATTAATGGAATATGACATCGCTAAAGCTGTAGCGTGTGCAAGCATATGTC 354
    |||
Db 241 TGCAGCGAATTAATGGAATATGACATCGCTAAAGCTGTAGCATGTGCAAGCATATGTC 300
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QY 355 AGTGACCAAGGCAATTAACAGCTGGGTGGCATGGAAAAGTCATTGTGAGAGCCATGACGTC 414
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Db 301 AGTGACCAAGGCAATTAACAGCTGGGTGGCATGGAAAAGTCATTGTGAGAGCCATGACGTC 360
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QY 415 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 444
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Db 361 AGCAGTTACGTTGAGGGTTGCACCCCTGTAA 390
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Job time : 1383 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 04:49:56 ; Search time 179 Seconds

(without alignments)  
5585.962 Million cell updates/sec

Title: US-09-978-199-1

Perfect score: 444  
Sequence: 1 atgaagctctcgtattctc.....ttgaggttcgacctgtaa 444

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	444	100.0	444	24	AA039128
2	444	100.0	459	11	AA005054
3	444	100.0	10130	24	AA039129
4	439	98.9	964	20	AAV08922
5	437.4	98.5	964	10	AAV08922
6	435.8	98.2	964	14	AA039092
7	280.6	63.2	1483	24	ABK64517
8	280.6	63.2	1494	11	AA003369
9	280.6	63.2	1496	10	AAV02386

10	280.6	63.2	1512	22	AA017725
11	280.6	63.2	1512	23	AA056881
12	280.6	63.2	1776	23	ABV24794
13	279	62.8	748	24	AB170110
14	270.4	60.9	490	8	AAV0949
15	269.2	60.6	435	10	AAV02054
16	269.2	60.3	447	8	AAV0943
17	267.8	60.3	447	24	AB137496
18	265.2	59.7	2467	24	AA039104
19	264.2	59.5	444	22	AA017740
20	257.4	58.0	1798	23	AA056076
21	250	56.3	657	21	AAV16339
22	239	53.8	390	8	AAV0944
23	222.6	50.1	614	22	AAV5437
24	187.8	42.3	449	11	AA003794
25	185.6	41.8	585	24	AB138017
26	185.4	41.8	464	12	AAQ10356
27	176.6	39.8	447	10	AAV09102
28	176.2	39.7	444	12	AAQ13590
29	175.4	39.5	399	11	AA003795
30	169.6	38.2	390	22	AA164878
31	163.8	36.9	390	7	AAV0206
32	163.6	36.8	233	24	ABK16005
33	162.6	36.6	396	10	AAV09066
34	162.6	36.6	396	11	AAQ06558
35	162.6	36.6	396	11	AAQ05669
36	157.8	35.5	418	7	AAV09053
37	157.8	35.5	394	8	AAV0537
38	157.2	35.4	394	7	AAV0214
39	157.2	35.4	394	9	AAV01354
40	157.2	35.4	394	9	AAV01284
41	157.2	35.4	394	9	AAV01447
42	157.2	35.4	394	10	AAV02359
43	157.2	35.4	427	9	AAV01735
44	157	35.4	706	24	ABO58989
45	156.2	33.2	396	14	AAQ52670

## ALIGNMENTS

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KW	Bovine; viral vector; transgenic plant; lysozyme; antibacterial;		
KW	Pierce's disease; PD; Xylella fastidiosa bacterium infection;		
KW	anti-Xylella reagent; grapevine; gene; ds.		
OS	Bos sp.		
FX			
FT	Key	Location/Qualifiers	
FT	CDS	1..444	
FT		/product="Bovine lysozyme"	
PN	WO200233041-A2.		
PD	25-APR-2002.		
XX			
XX	17-OCT-2001; 2001WO-US32147.		
XX	18-OCT-2000; 2000US-240967P.		
XX	(LARG-) LARGE SCALE BIOLOGY CORP.		
XX	Pogue G, Velichko S;		
PI			

Human macrophage-e  
DNA encoding novel  
Human prostate exp  
Pancreas cancer re  
Sequence encoding  
Sequence of human  
Human colon tumour  
Human lung-specific  
Human macrophage-e  
DNA encoding novel  
Human colon cancer  
Sequence encoding  
Nucleotide sequenc  
Synthetic human ly  
Human colon tumour  
Synthetic human ly  
Human lysozyme DNA  
Avian lysozyme sig  
Mutant human lysoz  
Human lysozyme cod  
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Human lung tumour  
Sequence of natura  
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Human lysozyme  
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Synthetic human ly  
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Sequence encoding  
Modified DNA sequ  
Sequence of the Ta  
TagI - XhoI fragme  
pRIT-2 human lys  
Human colon cancer  
Mutant human lysoz







Db 444 TGAGGGTTGCACCTGTAA 462

RESULT 7  
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ID ABK64517 standard; DNA; 1483 BP.  
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DE 18-JUN-2002 (first entry)  
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XX Human benign prostatic hyperplasia gene #412.  
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XX Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX W0200212440-A2.  
XX  
XX 14-FEB-2002.  
XX  
XX 07-AUG-2001; 2001WO-US24708.  
XX  
XX 07-AUG-2000; 2000US-223323P.  
XX 05-JUN-2001; 2001US-0873319.  
XX  
XX (GENE-) GENE LOGIC INC.  
XX (NISB) JAPAN TOBACCO INC.  
XX  
XX Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;  
XX  
XX WPI; 2002-257476/30.  
XX  
XX Identifying drugs for and diagnosing benign prostatic hyperplasia, by  
XX detecting expression levels of one or more genes in prostate cells from  
XX patient that are differentially regulated compared to normal prostate  
XX cells \_  
XX  
XX Disclosure; Page 241: 444pp; English.  
XX  
XX The invention relates to a method of diagnosing (I) the onset or  
XX progression of benign prostatic hyperplasia (BPH), or screening (II) for  
XX or identifying an agent that modulates the onset or progression of BPH.  
XX The method is based on changes in gene expression in BPH tissue isolated  
XX from patients exhibiting different clinical states of prostate  
XX hyperplasia as compared to normal prostate tissue. (I) comprises  
XX detecting the expression levels of one or more genes in prostate cells  
XX from the subject that are differentially regulated compared to normal  
XX prostate cells. (II) comprises preparing a first gene expression profile  
XX of BPH cells or BPH-like cell population, exposing the cells to the  
XX agent, preparing a second gene expression profile of the agent exposed  
XX cells, and comparing the first and second gene expression profiles.  
XX (I) is useful for diagnosing the onset or progression of BPH. (II) is  
XX useful for identifying an agent that modulates the onset or progression  
XX of BPH. The methods are useful to present information identifying  
XX the expression level in a tissue or cells, by comparing the expression  
XX level of genes given in the specification in the tissue or cells to the  
XX level of expression of gene in the database, and displaying the  
XX expression levels of at least one gene in the tissue or cell sample  
XX compared to the expression level in BPH. Agents using (II) are useful for  
XX treating BPH or prostate cancer. ABK64106-ABK64860 represent human  
XX benign prostatic hyperplasia gene sequences of the invention.  
XX  
XX Sequence 1483 BP; 432 A; 298 C; 309 G; 444 T; 0 other;  
XX

Query Match 63.2%; Score 280.6; DB 24; Length 1483;  
Best Local Similarity 78.3%; Pred. No. 1.8e-76;  
Matches 350; Conservative 0; Mismatches 94; Indels 3; Gaps 1

1 ATGAAGGCTCGTATTCCTGGGGTTTCTCTTCCTTGTCGTCGTCGAAGCAAGGTC 60  
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14 ATGAAGGCTCATTTGTTGGGGCTTGTCTCTTTCTTTGTTACGGTCCAGGCAAGGTC 73

QY 61 TTGAGAGATGTAGCTTCCAGAACTCTGAGAACTTGAGCTGAGCGCTATTAAGGA 120  
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 Db 374 CCACAAGGCAATGAGCATGGTGGCATGAGAAATCGTTGTCAAAACAGAGATGTCGGT 433  
 QY 418 AGTTACGTTGAGGGTGCACCCCTGTAA 444  
 Db 434 CAGTATGTTCAAGGTGTGTGGAGTGTAA 460  
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 AC AAQ03369;  
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 DE  
 KW Transgenic animal; enzyme; ss.  
 OS Homo sapiens.  
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 FH Key Location/Qualifiers  
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 XX JP02005879-A.  
 XX 10-JAN-1990.  
 PD  
 XX 21-JUN-1988; 88JP-0151106.  
 PF  
 XX 21-JUN-1988; 88JP-0151106.  
 PR  
 XX (TAKE ) TAKEDA CHEMICAL IND KK.  
 PA WPI; 1990-053916/08.  
 DR P-PSDB; AAR06108.  
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 PT Human lysozyme gene -  
 XX useful promoter for genetic expression of animal culturing cell  
 XX ; Fig 4-1 to 4-3 Pages 834-835; 13pp; Japanese.  
 PS  
 CC Human lysozyme DNA can be used to obtain transgenic animals, e.g. mice.  
 CC It can also be produced by culturing animal cells, and it can  
 CC promote the genetic expression of these animal cells.  
 XX Sequence 1494 BP; 441 A; 298 C; 309 G; 446 T; 0 other;

Query Match 63.2%; Score 280.6; DB 11; Length 1494;  
 Best Local Similarity 78.3%; Pred. No. 1.8e-76;  
 Matches 350; Conservative 0; Mismatches 94; Indels 3; Gaps 1;  
 QY 1 ATGAGGCTCTGCTGTTATTTCTGGGGTTCTCTTCTCTTCTGCTGCTCCAAAGCAAGCTC 60  
 Db 14 ATGAGGCTCTGCTGTTATTTCTGGGGTTCTCTTCTCTTCTGCTGCTCCAAAGCAAGCTC 73  
 QY 61 TTTGAGAGTGTGAGCTTGGCCAGAACTCTGAAAGAACTTGAGCTGAGAGGCTATTAAGGA 120  
 Db 74 TTTGAAAGGTGTGAGTTGGCCAGAACTCTGAAAGAACTTGGAATGATGCTACAGGGGA 133  
 QY 121 GTGAGCGTGGCAACTGGTGTGTTTGACCAATGGGAAAGCACTTATTAACAAAAAGCT 180  
 Db 134 ATCAGCGCTAGCAAACTGGATGTGTTGGCCAAATGGGAGATGTTCAACACACAGAGCT 193  
 QY 181 ACAAACTACATCTTACAGTGAAGCACTGATTTATTTGATTCAGATCAACAGCAAA 240  
 Db 194 ACAAACTACATCTTACAGTGAAGCACTGATTTATTTGATTCAGATCAACAGAGCT 253  
 QY 241 TGTGGTGTATGATGAGCAAAACCCCTAATGACAGTTCAGCTGATTCCTGAGC 300  
 Db 254 TACTGTGTATGATGAGCAAAACCCCTAATGACAGTTCAGCTGATTCCTGAGC 313  
 QY 301 GAATTAATGAAATGATGATGCAATGCAATGCTGAGCGTGCAGAAAGCATATTGACATGA- 359  
 Db 314 GCTTGTGCTGCAAGTAACTGATGCTGATGCTGATGCTGCAAAAGAGGTTGCGCGAT 373  
 QY 360 --GCAAGGCAATACAGCTGGTGGCATGAGAAAGTCAATGTCGAGCATGACGTCAGC 417  
 Db 374 CCACAAGGCAATGAGCATGGTGGCATGAGAAATCGTTGTCAAAACAGAGATGTCGGT 433  
 QY 418 AGTTACGTTGAGGGTGCACCCCTGTAA 444  
 Db 434 CAGTATGTTCAAGGTGTGTGGAGTGTAA 460  
 RESULT 9  
 AAN92386  
 ID AAN92386 standard; DNA; 1496 BP.  
 AC AAN92386;  
 XX 03-JUN-1990 (first entry)  
 DT  
 XX DNA coding for the signal peptide and mature protein of human lysozyme  
 DE (HL).  
 KW Human lysozyme; HL; bacterial infection.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT sig\_peptide 14..67  
 FT /\*tag= a  
 FT mat\_peptide 68..457  
 FT /\*tag= b  
 FT CDS 14..460  
 FT /\*tag= c  
 XX JP01074989-A.  
 XX 20-MAR-1989.  
 PD  
 XX 16-SEP-1987; 87JP-0229752.  
 PF  
 XX 16-SEP-1987; 87JP-0229752.  
 PR  
 XX (TAKE ) TAKEDA CHEMICAL IND KK.  
 PA WPI; 1989-127529/17.  
 DR P-PSDB; AAP93510.  
 XX













GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 05:03:49 ; Search time 1138 Seconds  
(without alignments)  
6318.802 Million cell updates/sec

Title: US-09-978-199-1

Perfect score: 444  
Sequence: 1 atgaagctctcgttatctc.....ttgaggttcacacctgtaa 444

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	100.0	453	13	BG937925
2	444	100.0	462	13	BG938107
3	444	100.0	463	13	BG938377
4	444	100.0	464	13	BG938413
5	444	100.0	469	13	BG938112
6	444	100.0	476	13	BG937589

7	444	100.0	476	13	BG938203	BG938203
8	444	100.0	478	13	BG937601	BG937601
9	444	100.0	481	13	BG937832	BG937832
10	444	100.0	482	13	BG937936	BG937936
11	444	100.0	484	13	BG937881	BG937881
12	444	100.0	485	13	BG938200	BG938200
13	444	100.0	486	13	BG937882	BG937882
14	444	100.0	486	13	BG938101	BG938101
15	444	100.0	487	13	BG938250	BG938250
16	444	100.0	491	13	BG937866	BG937866
17	444	100.0	493	13	BG937861	BG937861
18	444	100.0	494	13	BG938345	BG938345
19	444	100.0	497	13	BG937747	BG937747
20	444	100.0	497	13	BG938042	BG938042
21	444	100.0	498	13	BG937670	BG937670
22	444	100.0	502	13	BG937865	BG937865
23	444	100.0	503	13	BG937991	BG937991
24	444	100.0	513	13	BG938316	BG938316
25	444	100.0	525	10	AM654651	AM654651
26	443	99.8	485	13	BG938044	BG938044
27	443	99.8	488	13	BG937749	BG937749
28	442.4	99.6	461	13	BG937779	BG937779
29	439	98.9	448	13	BG938303	BG938303
30	439	98.9	484	13	BG938144	BG938144
31	438	98.6	453	13	BG937445	BG937445
32	437	98.4	456	13	BG938205	BG938205
33	436.4	98.3	453	13	BG937506	BG937506
34	433.4	97.6	454	13	BG938097	BG938097
35	433.4	97.6	460	13	BG937777	BG937777
36	433	97.5	460	13	BG937768	BG937768
37	433	97.5	462	13	BG938068	BG938068
38	433	97.5	498	13	BG937733	BG937733
39	433	97.5	503	13	BG937795	BG937795
40	432	97.3	448	13	BG937811	BG937811
41	432	97.3	450	13	BG938187	BG938187
42	432	97.3	470	13	BG938401	BG938401
43	432	97.3	487	13	BG938403	BG938403
44	431.4	97.2	463	13	BG937730	BG937730
45	431	97.1	453	13	BG937415	BG937415

## ALIGNMENTS

RESULT 1  
LOCUS BG937925 453 bp mRNA linear EST 11-JUN-2001  
DEFINITION IABO09H04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA  
sequence.  
ACCESSION BG937925  
VERSION BG937925.1 GI:14337297  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE  
1 (bases 1 to 453)  
Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.  
CDNA's from bovine abomasum tissue  
Unpublished (2001)  
CONTACT: Dr. Stephen Moore  
Beef Genomics Laboratory  
Dept of AFNS, University of Alberta  
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0169  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA  
) in main database at high score of 898.0 and E-value of 0.0  
PCR PRIMERS  
FORWARD: M13 Forward  
BACKWARD: M13 Reverse



KEYWORDS	EST.
SOURCE	COW.
ORGANISM	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
AUTHORS	Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
TITLE	CDNA's from bovine abomasum tissue
JOURNAL	Unpublished (2001)
COMMENT	Contact: Dr. Stephen Moore Beef Genomics Laboratory Dept of AFNS, University of Alberta 410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169 Fax: 780 492 4265 Email: smoores@afns.ualberta.ca The sequence best matches gb:BOVLYZM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 918.0 and E-value of 0.0
FEATURES	PCR Primers FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer High quality sequence stop: 463 POLY-A-No.
SOURCE	Location/Qualifiers 1. 463 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="Bovine Abomasum cDNA Library" /sex="Two males and one female mixed" /tissue_type="Gastrointestinal tissue (GIT)" /cell_type="Epithelial" /dev_stage="Young adult" /lab_host="XL1-BlueMRF"-strain /note="Organ: Abomasum; Vector: Uni-ZAPXR; Site_1: Ecor I; Site_2: Xho I"
BASE COUNT	133 a 91 c 119 g 120 t
ORIGIN	
Query Match	100.0%; Score 444; DB 13; Length 463;
Best Local Similarity	100.0%; Pred. No. 4,9e-125;
Matches 444;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	ATGAAGGCTCTCGTTATTCGTGGGGTTTCCTCTTCCTTCCTGTCGCTGCAAGGAGGCTC 60
20	ATGAAGGCTCTCGTTATTCGTGGGGTTTCCTCTTCCTTCCTGTCGCTGCAAGGAGGCTC 79
61	TTTGAGAGATGTGAGCTTGCCAGAACTGGAAGAACTTGACAGTGGAGCGCTATTAAAGGA 120
80	TTTGAGAGATGTGAGCTTGCCAGAACTGGAAGAACTTGACAGTGGAGCGCTATTAAAGGA 139
121	GTCACCCGGGCAAACTGGTGTGTGTGACCAAAATGGGAAGCAGTTATAACCAAAAGCT 180
140	GTCACCCGGGCAAACTGGTGTGTGTGACCAAAATGGGAAGCAGTTATAACCAAAAGCT 199
181	ACAAACTCAATTCCTAGCAGTGAAGAAAGCACTGTTATGGGATATTTCAGATCAACAGCAA 240
200	ACAAACTCAATTCCTAGCAGTGAAGAAAGCACTGTTATGGGATATTTCAGATCAACAGCAA 259
241	TGTTGGTGTATATGATGCGCAAAACCCCTTAATGAGATTGAAGCGCTGCATGTATCTCGACG 300
260	TGTTGGTGTATATGATGCGCAAAACCCCTTAATGAGATTGAAGCGCTGCATGTATCTCGACG 319
301	GAATTAATGAGAAATGACATGGCTTAAGCTGAGGTGGCAAAACATATTGTGCTGAG 360
320	GAATTAATGAGAAATGACATGGCTTAAGCTGAGGTGGCAAAACATATTGTGCTGAG 379
361	CAAGGCAATTACAGCCCTGGGTGGCAAGAAAGTCATTGTGAGACATGACGTCAAGCAGT 420
380	CAAGGCAATTACAGCCCTGGGTGGCAAGAAAGTCATTGTGAGACATGACGTCAAGCAGT 439
421	TACGTTGAGGGTTGCACCCCTGTAA 444

Db	440	TACGTTGAGGTTGCACCCCTGTAA	463
RESULT 4	BG38413	464 bp	mRNA linear EST 11-JUN-2001
LOCUS	BG38413		
DEFINITION	1AB007G10 Bovine Abdomasum cDNA Library Bos taurus cDNA 5', mRNA		
ACCESSION	BG38413		
VERSION	BG38413.1	GI:14337785	
KEYWORDS	EST.		
SOURCE	cow.		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 464)		
TITLE	Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y., and Li, G.		
JOURNAL	CDNA's from bovine abdomasum tissue		
COMMENT	Unpublished (2001)		
	Contact: Dr. Stephen Moore		
	. Beef Genomics Laboratory		
	Dept of AFNS, University of Alberta		
	410 AgriFor. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada		
	Tel: 780 492 0169		
	Fax: 780 492 4265		
	Email: smoores@atns.ualberta.ca		
	The sequence best matches gb:BOV12YM7A (Bos taurus lysozyme 7A mRNA		
	) in main database at high score of 920.0 and E-value of 0.0		
	PCR primers		
	FORWARD: M13 Forward		
	BACKWARD: M13 Reverse		
	Seq primer: T3 primer		
	POLYA=NO.		
FEATURES	Location/Qualifiers		
source	1..464		
	/organism="Bos taurus"		
	/db_xref="taxon:9913"		
	/clone_lib="Bovine Abdomasum cDNA library"		
	/sex="Two males and one female mixed"		
	/tissue_type="Gastrointestinal tissue (GIT)"		
	/cell_type="Epithelial"		
	/dev_stage="Young adult"		
	/lab_host="XL1-BlueMRF", strain"		
	/note="Organ: Abdomasum; Vector: Uni-ZAPXR; Site_1: Ecor		
	I; Site_2: Xho I"		
BASE COUNT	132 a 92 c 121 g 119 t		
ORIGIN			
Query Match	100.0%; Score 444; DB 13; Length 464;		
Best Local Similarity	100.0%; Pred. No. 4.9e-125;		
Matches	444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ATGAAGCGCTCGTATTCTGGGGTTTCTCTTCCTTCTGTCGCTGTCCAGGCAAGTC 60		
DB	14 ATGAAGCGCTCGTATTCTGGGGTTTCTCTTCCTTCTGTCGCTGTCCAGGCAAGTC 73		
QY	61 TTGGAGAGATGAGACTTGCCAGACTCGAAGAACTTGAGACTGGAGCTATAAGGA 120		
DB	74 TTGGAGAGATGAGACTTGCCAGACTCGAAGAACTTGAGACTGGAGCTATAAGGA 133		
QY	121 GTCAGCGCTGGCAAACTGGTGTGTTGTAACCAATGGGAAGCAGTTATTAACCAAAAGCT 180		
DB	134 GTCAGCGCTGGCAAACTGGTGTGTTGTAACCAATGGGAAGCAGTTATTAACCAAAAGCT 193		
QY	181 ACAAACTCAATCCTAGCAGTGAAGCACTGATTTTGGGATTTTCAATCAACAGCAA 240		
DB	194 ACAAACTCAATCCTAGCAGTGAAGCACTGATTTTGGGATTTTCAATCAACAGCAA 253		
QY	241 TGGTGTGTAATGAAGGCAAAACCCCTATGAGAGTGAAGGCTGCATGATACCGCAGC 300		
DB	254 TGGTGTGTAATGAAGGCAAAACCCCTATGAGAGTGAAGGCTGCATGATACCGCAGC 313		

QY 301 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGCGTGAAGCATATTGTCAGT 360  
 |||||||  
 DB 314 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGCGTGAAGCATATTGTCAGT 373  
 |||||||  
 QY 361 CAAGCATTTACAGCTGGTGGCATGGAAGTCAATGTCGACCATGACGTCAGT 420  
 |||||||  
 DB 374 CAAGCATTTACAGCTGGTGGCATGGAAGTCAATGTCGACCATGACGTCAGT 433  
 |||||||  
 QY 421 TACGTTGAGGCTTGCACCTGTAA 444  
 |||||||  
 DB 434 TACGTTGAGGCTTGCACCTGTAA 457  
 |||||||

RESULT 5  
 BG938112 469 bp mRNA linear EST 11-JUN-2001  
 LOCUS 1AB011D12 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA  
 DEFINITION  
 ACCESSION BG938112  
 VERSION BG938112  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 469)  
 Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.  
 cDNA's from bovine abomasum tissue  
 Unpublished (2001)  
 CONTACT: Dr. Stephen Moore  
 . Beef Genomics Laboratory  
 Dept of AFNS, University of Alberta  
 410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 Tel: 780 492 0169  
 Fax: 780 492 4265  
 Email: smoores@afns.ualberta.ca  
 The sequence best matches gb:BOVLZYW7A (Bos taurus lysozyme 7A mRNA  
 ) in main database at high score of 930.0 and E-value of 0.0  
 PCR PRIMERS  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 469  
 POLYA-No.

FEATURES  
 source location/Qualifiers  
 1..469  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="Bovine Abomasum cDNA Library"  
 /sex="Two males and one female mixed"  
 /tissue\_type="Gastrointestinal tissue (GIT)"  
 /cell\_type="Epithelial"  
 /dev\_stage="Young adult"  
 /lab\_host="X11-BlueRF"-strain"  
 /note="Organ: Abomasum; Vector: Uni-ZAPXR; Site\_1: EcoR  
 I; Site\_2: Xho I"

BASE COUNT 133 a 92 c 123 g 121 t  
 ORIGIN

Query Match 100.0%; Score 444; DB 13; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 5e-125;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTCTCTATATCTGGGGTTCTCTCTTCTGTCGCTGCCAAGGCAAGTTC 60  
 |||||||  
 DB 17 ATGAGGCTCTCTATATCTGGGGTTCTCTCTTCTGTCGCTGCCAAGGCAAGTTC 76  
 |||||||  
 QY 61 TTGAGAGATGTAGCTGGCAGACTGGAAGAACTGAGCTGAGCGGCTATAGGGA 120  
 |||||||  
 DB 77 TTGAGAGATGTAGCTGGCAGACTGGAAGAACTGAGCGGCTATAGGGA 136  
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QY 121 GTCAGCTGGCAACACTGTTGTGTTTGACCAATGGGAAGACGTTATACCAAACT 180  
 |||||||  
 DB 137 GTCAGCTGGCAACACTGTTGTGTTTGACCAATGGGAAGACGTTATACCAAACT 196  
 |||||||  
 QY 181 ACAAACTACAACTCTAGCAGTGAAGACATGATTAATGGATTTTCAGTCAACGCAAA 240  
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 DB 197 ACAAACTACAACTCTAGCAGTGAAGACATGATTAATGGATTTTCAGTCAACGCAAA 256  
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 QY 241 TGGTGTGTTAATGATGGCAAAACCCCTAATGCAATTGACGCTGTCATGTCGACG 300  
 |||||||  
 DB 257 TGGTGTGTTAATGATGGCAAAACCCCTAATGCAATTGACGCTGTCATGTCGACG 316  
 |||||||  
 QY 301 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGCGTGAAGCATATTGTCAGT 360  
 |||||||  
 DB 317 GAATTAATGAAATGACATCGCTAAAGCTGTACGCTGCGTGAAGCATATTGTCAGT 376  
 |||||||  
 QY 361 CAAGCATTTACAGCTGGTGGCATGGAAGTCAATGTCGACCATGACGTCAGT 420  
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 DB 377 CAAGCATTTACAGCTGGTGGCATGGAAGTCAATGTCGACCATGACGTCAGT 436  
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 QY 421 TACGTTGAGGCTTGCACCTGTAA 444  
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 DB 437 TACGTTGAGGCTTGCACCTGTAA 460  
 |||||||

RESULT 6  
 BG937589 476 bp mRNA linear EST 11-JUN-2001  
 LOCUS 1AB003C3 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA  
 DEFINITION  
 ACCESSION BG937589  
 VERSION BG937589  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 476)  
 Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.  
 cDNA's from bovine abomasum tissue  
 Unpublished (2001)  
 CONTACT: Dr. Stephen Moore  
 . Beef Genomics Laboratory  
 Dept of AFNS, University of Alberta  
 410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 Tel: 780 492 0169  
 Fax: 780 492 4265  
 Email: smoores@afns.ualberta.ca  
 The sequence best matches gb:BOVLZYW7A (Bos taurus lysozyme 7A mRNA  
 ) in main database at high score of 944.0 and E-value of 0.0  
 PCR PRIMERS  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 476  
 POLYA-No.

FEATURES  
 source location/Qualifiers  
 1..476  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="Bovine Abomasum cDNA Library"  
 /sex="Two males and one female mixed"  
 /tissue\_type="Gastrointestinal tissue (GIT)"  
 /cell\_type="Epithelial"  
 /dev\_stage="Young adult"  
 /lab\_host="X11-BlueRF"-strain"  
 /note="Organ: Abomasum; Vector: Uni-ZAPXR; Site\_1: EcoR  
 I; Site\_2: Xho I"

BASE COUNT 135 a 94 c 122 g 125 t  
 ORIGIN  
 Query Match 100.0%; Score 444; DB 13; Length 476;



PCR primers  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 478  
 POLY-A-No.

## FEATURES

source

Location/Qualifiers  
 1..478  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="Bovine Abomasum cDNA Library"  
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 /tissue\_type="Gastrointestinal tissue (GIT)"  
 /cell\_type="Epithelial"  
 /dev\_stage="Young adult"  
 /lab\_host="XLI-BlueMRF-strain"  
 /note="Organ: Abomasum; Vector: Uni-ZAPXR; Site\_1: EcoR  
 I; Site\_2: Xho I"

BASE COUNT 135 a 95 c 123 g 125 t

ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 444; DB 13; Length 478;  
 Pred. No. 5e-125;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAGGCTCTCGTTATTCCTGCGGTTCTCTCCCTTCTGCGCTGCCAAGGCAAGTC 60  
 12 ATGAAGGCTCTCGTTATTCCTGCGGTTCTCTCCCTTCTGCGCTGCCAAGGCAAGTC 71  
 61 TTGAGAGATGTGAGCTTCCGAGACTGTGAAGAACTTGAGCTGAGCGCTATTAAGGA 120  
 72 TTGAGAGATGTGAGCTTCCAGAACTGTGAAGAACTTGAGCTGAGCGCTATTAAGGA 131  
 121 GTCAGCGCTGCAAACTGTTGTTGTTGACCAATGGGAAGAGATTAACCAAAAGT 180  
 132 GTCAGCGCTGCAAACTGTTGTTGTTGACCAATGGGAAGAGATTAACCAAAAGT 191  
 181 ACAACTACATCTTCAAGCTGAGTGAAGCACTGATTAATGGAATTTTCAGATCAACAGCAA 240  
 192 ACAACTACATCTTCAAGCTGAGTGAAGCACTGATTAATGGAATTTTCAGATCAACAGCAA 251  
 241 TGGTGGTAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 300  
 252 TGGTGGTAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 311  
 301 GAATTAATGAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 360  
 312 GAATTAATGAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 371  
 361 CAAGGCTTACAGCGCTGAGTGAAGAAAGTATGTCGAGACCATGAGCTGACAGT 420  
 372 CAAGGCTTACAGCGCTGAGTGAAGAAAGTATGTCGAGACCATGAGCTGACAGT 431  
 421 TACGTTAGAGGTTGACACCTGTAA 444  
 432 TACGTTAGAGGTTGACACCTGTAA 455

RESULT 9  
 BG937832 481 bp mRNA linear EST 11-JUN-2001  
 LOCUS BG937832  
 DEFINITION 1Ab007603 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA  
 sequence.  
 ACCESSION BG937832  
 VERSION BG937832.1 GI:14337204  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 Bos taurus  
 Cow.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.

REFERENCE  
 1 (bases 1 to 481)  
 Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.

TITLE  
JOURNAL  
COMMENT

CDNA's from bovine abomasum tissue  
 Unpublished (2001)  
 Contact: Dr. Stephen Moore  
 Beel Genomics Laboratory  
 Dept of AFNS, University of Alberta  
 410 April/Fox, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 Tel: 780 492 0169  
 Fax: 780 492 4265  
 Email: smoores@afns.ualberta.ca  
 The sequence best matches gb:BOVUZLYM7A (Bos taurus lysozyme 7A mRNA  
 ) in main database at high score of 954.0 and E-value of 0.0  
 PCR Primers  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 481  
 POLY-A-No.

## FEATURES

source

Location/Qualifiers  
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 /clone\_lib="Bovine Abomasum cDNA Library"  
 /sex="Two males and one female mixed"  
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 /lab\_host="XLI-BlueMRF-strain"  
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 I; Site\_2: Xho I"

BASE COUNT 136 a 95 c 124 g 126 t

ORIGIN

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Best Local Similarity 100.0%; Score 444; DB 13; Length 481;  
 Pred. No. 5e-125;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAGGCTCTCGTTATTCCTGCGGTTCTCTCCCTTCTGCGCTGCCAAGGCAAGTC 60  
 16 ATGAAGGCTCTCGTTATTCCTGCGGTTCTCTCCCTTCTGCGCTGCCAAGGCAAGTC 75  
 61 TTGAGAGATGTGAGCTTCCGAGACTGTGAAGAACTTGAGCTGAGCGCTATTAAGGA 120  
 76 TTGAGAGATGTGAGCTTCCAGAACTGTGAAGAACTTGAGCTGAGCGCTATTAAGGA 135  
 121 GTCAGCGCTGCAAACTGTTGTTGTTGACCAATGGGAAGAGATTAACCAAAAGT 180  
 136 GTCAGCGCTGCAAACTGTTGTTGTTGACCAATGGGAAGAGATTAACCAAAAGT 195  
 181 ACAACTACATCTTCAAGCTGAGTGAAGCACTGATTAATGGAATTTTCAGATCAACAGCAA 240  
 196 ACAACTACATCTTCAAGCTGAGTGAAGCACTGATTAATGGAATTTTCAGATCAACAGCAA 255  
 241 TGGTGGTAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 300  
 256 TGGTGGTAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 315  
 301 GAATTAATGAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 360  
 316 GAATTAATGAAATGATGCAAAACCCCTAATGAGTGAAGCTGAGCGCTGATATCTGACG 375  
 361 CAAGGCTTACAGCGCTGAGTGAAGAAAGTATGTCGAGACCATGAGCTGACAGT 420  
 376 CAAGGCTTACAGCGCTGAGTGAAGAAAGTATGTCGAGACCATGAGCTGACAGT 435  
 421 TACGTTAGAGGTTGACACCTGTAA 444  
 436 TACGTTAGAGGTTGACACCTGTAA 459

RESULT 10  
 BG937936 482 bp mRNA linear EST 11-JUN-2001  
 LOCUS BG937936  
 DEFINITION 1Ab008E01 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA



QY 241 TGGTGTATGATGAGCAAAACCCCTAATGAGCGCTGTCATGATCTGCAGC 300  
 DB 254 TGGTGTATGATGAGCAAAACCCCTAATGAGCGCTGTCATGATCTGCAGC 313  
 QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGAGCGTGCCAAAGCATATTTGCTAGTGA 360  
 DB 314 GAATTAATGAAAAATGACATCGCTAAAGCTGAGCGTGCCAAAGCATATTTGCTAGTGA 373  
 QY 361 CAAGGCAATTACGCTGGTGGCATGGAAGATCATTTGTCAGACATGACATGACATGACAT 420  
 DB 374 CAAGGCAATTACGCTGGTGGCATGGAAGATCATTTGTCAGACATGACATGACATGACAT 433  
 QY 421 TACGTTGAGGGTTGCACCCCTGTAA 444  
 DB 434 TACGTTGAGGGTTGCACCCCTGTAA 457

RESULT 12  
 BG938200 485 bp mRNA linear EST 11-JUN-2001  
 LOCUS 1AB013G04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA  
 DEFINITION  
 ACCESSION BG938200  
 VERSION BG938200.1 GI:14337572  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Bos taurus  
 Cow.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 485)  
 Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.  
 CDNA's from bovine abomasum tissue  
 Unpublished (2001)  
 JOURNAL  
 COMMENT  
 CONTACT: Dr. Stephen Moore  
 Beef Genomics Laboratory  
 Dept of AFNS, University of Alberta  
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 Tel: 780 492 0169  
 Fax: 780 492 4265  
 Email: smoores@afns.ualberta.ca  
 The sequence best matches gb:BOVL2YM7A (Bos taurus lysozyme 7A mRNA  
 ) in main database at high score of 961.0 and E-value of 0.0  
 PCR PRIMERS  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 485  
 POLYA-NO.

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 /tissue\_type="Gastrointestinal tissue (GIT)"  
 /cell\_type="Epithelial"  
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 /lab\_host="XLI-BlueMRF-strain"  
 /note="Organ: Abomasum; Vector: Uni-22APXR; Site:1: EcoR  
 I; Site\_2: Xho I"

BASE COUNT 137 a 97 c 123 g 128 t

Query Match 100.0%; Score 444; DB 13; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 5e-125;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTGCTATTCCTGAGGGTTCTCTCTCTCTGCTGCTGCCAAGGCAAGGTC 60  
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QY 61 TTGAGAGATGTGAGCTTGGCCAGACTCTGAAGAAACTTGGACGTGAGCGGTATAGGGA 120  
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 QY 121 GTACCGCTGGCAAACTGGTTGTGTTGAACCAAAATGGAAAGCAGTTATMACAAAAAGCT 180  
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 DB 255 TGGTGTGTAATGATGAGCAAAACCCCTAATGAGCGCTGTCATGATCTGCAGC 314  
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 DB 315 GAATTAATGAAAAATGACATCGCTAAAGCTGAGCGTGCCAAAGCATATTTGCTAGTGA 374  
 QY 361 CAAGGCAATTACGCTGGTGGCATGGAAGATCATTTGTCAGACATGACATGACATGACAT 420  
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 QY 421 TACGTTGAGGGTTGCACCCCTGTAA 444  
 DB 435 TACGTTGAGGGTTGCACCCCTGTAA 458

RESULT 13  
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 LOCUS 1AB009C07 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA  
 DEFINITION  
 ACCESSION BG937882  
 VERSION BG937882.1 GI:14337254  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Bos taurus  
 Cow.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 486)  
 Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.  
 CDNA's from bovine abomasum tissue  
 Unpublished (2001)  
 JOURNAL  
 COMMENT  
 CONTACT: Dr. Stephen Moore  
 Beef Genomics Laboratory  
 Dept of AFNS, University of Alberta  
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 Tel: 780 492 0169  
 Fax: 780 492 4265  
 Email: smoores@afns.ualberta.ca  
 The sequence best matches gb:BOVL2YM7A (Bos taurus lysozyme 7A mRNA  
 ) in main database at high score of 963.0 and E-value of 0.0  
 PCR PRIMERS  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 486  
 POLYA-NO.

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 location/Qualifiers  
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 /sex="Two males and one female mixed"  
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 /cell\_type="Epithelial"  
 /dev\_stage="Young adult"  
 /lab\_host="XLI-BlueMRF-strain"  
 /note="Organ: Abomasum; Vector: Uni-22APXR; Site:1: EcoR  
 I; Site\_2: Xho I"

QY 1 ATGAAGGCTCTGCTATTCCTGAGGGTTCTCTCTCTCTGCTGCTGCCAAGGCAAGGTC 60  
 DB 15 ATGAAGGCTCTGCTATTCCTGAGGGTTCTCTCTCTCTCTGCTGCTGCCAAGGCAAGGTC 74

ORIGIN	BASE COUNT	137 a	97 c	124 g	128 t
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Best Local Similarity	100.0%;	Pred. No. 5e-125;			
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Db	16	ATGAAGCCTCCGTTATTTCTGGGGTTCTCTCTCTTTCTGTCGCTGTCAGGGAAGTGC	75		
OY	61	TTTGAGAGATGTGAGCTTGGCCAGACTGTGAAAGCTTGAGCTGAGCGCTATAGGGA	120		
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OY	121	GTCAGCCTGGCAAACTGGTGTGTGTTGACCAATAGGGAAGCACTTTAATACAAAAGCT	180		
Db	136	GTCAGCCTGGCAAACTGGTGTGTGTTGACCAATAGGGAAGCACTTTAATACAAAAGCT	195		
OY	181	ACAAACTACATCTCTAGCAGTGAAGAGCACTGATTTATGGATTTTCAGATCAACAGCAA	240		
Db	196	ACAAACTACATCTCTAGCAGTGAAGAGCACTGATTTATGGATTTTCAGATCAACAGCAA	255		
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Db	256	TGTGTGTGTATATGATGCGAAACCCCTTATGCAAGTGAAGCTGTATGTTCTGCAAGC	315		
OY	301	GAATTAATGAAATATGACATGCTTAAAGCTTAGCGTGTGCAAGACATATTGTAGTAG	360		
Db	316	GAATTAATGAAATATGACATGCTTAAAGCTTAGCGTGTGCAAGACATATTGTAGTAG	375		
OY	361	CAAAGCATTTACAGCTGGGTGGCATGTGAAAGTCAATGTGAGACCATGAGCTGACAGT	420		
Db	376	CAAAGCATTTACAGCTGGGTGGCATGTGAAAGTCAATGTGAGACCATGAGCTGACAGT	435		
OY	421	TACGTTGAGGTTGCACCCCTGTA 444			
Db	436	TACGTTGAGGTTGCACCCCTGTA 459			
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LOCUS	1A001C10	Bovine Abomasum cDNA Library	Bos taurus cDNA 5', mRNA		
DEFINITION	Sequence.	BG938101			
ACCESSION	BG938101.1	GI:14337473			
VERSION	EST.				
KEYWORDS	cow.				
SOURCE	Bos taurus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. 1 (bases 1 to 486) Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y., and Li, G. cDNA's from bovine abomasum tissue Unpublished (2001)				
REFERENCE	CONTACT: Dr. Stephen Moore				
AUTHORS	Beef Genomics Laboratory				
TITLE	Dept of AFNS, University of Alberta				
JOURNAL	410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada				
COMMENT	Tel: 780 492 0169				
	Fax: 780 492 4265				
	Email: smoores@afns.ualberta.ca				
	) In the sequence best matches gb:BOV1ZYM7A (Bos taurus lysosyme 7A mRNA)				
	PCR primers				
	FORWARD: M13 Forward				
	BACKWARD: M13 Reverse				
	Seg primer: T3 primer				
	High quality sequence stop: 486				
FEATURES	POLYA-No.				
	Location/Qualifiers				



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 05:28:27 ; Search time 42 Seconds

(without alignments)  
3242.011 Million cell updates/sec

Title: US-09-978-199-1

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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5: /cgn2\_6/pdata/1/lna/PC/US.COMB.seq:\*  
6: /cgn2\_6/pdata/1/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	439	98.9	964	US-07-798-223A-1	Sequence 1, Appl
2	250	56.3	657	US-09-385-982-344	Sequence 344, App
3	157.2	35.4	394	5182195-1	Patent No. 5182195
4	153	34.5	396	US-08-503-584-6	Sequence 6, Appl
5	122.2	27.5	586	US-08-385-590A-3	Sequence 3, Appl
6	122.2	27.5	586	US-09-021-520-3	Sequence 3, Appl
7	63.8	14.4	222	US-09-388-917-1	Sequence 1, Appl
8	63	14.4	222	US-09-388-917-1	Sequence 1, Appl
9	48.4	10.9	301	US-09-388-917-2	Sequence 1, Appl
10	43	9.7	7218	US-08-332-463-14	Sequence 14, Appl
11	41.2	9.3	396	US-08-385-590A-1	Sequence 1, Appl
12	41.2	9.3	396	US-09-021-520-1	Sequence 1, Appl
13	32.2	7.3	4374	US-08-449-644-3	Sequence 3, Appl
14	32.2	7.3	4374	US-08-087-244A-3	Sequence 3, Appl
15	32	7.2	2082	US-09-440-325A-2	Sequence 2, Appl
16	31.6	7.1	1676	US-08-336-165A-212	Sequence 212, App
17	31.4	7.1	1499	US-08-889-841B-24	Sequence 24, Appl
18	31.4	7.1	1499	US-08-889-841B-27	Sequence 27, Appl
19	31.4	7.1	3726	US-08-173-497-1	Sequence 1, Appl
20	31.4	7.1	3726	US-08-286-889-1	Sequence 1, Appl
21	31.4	7.1	3726	US-08-485-618-1	Sequence 1, Appl
22	31.4	7.1	3726	US-08-362-652-1	Sequence 1, Appl
23	31.4	7.1	3726	US-08-605-672-1	Sequence 1, Appl
24	31.4	7.1	3726	US-08-482-293A-1	Sequence 1, Appl
25	31.4	7.1	3726	US-08-943-363-1	Sequence 1, Appl
26	31.4	7.1	3726	US-09-193-043-1	Sequence 1, Appl
27	31.4	7.1	3726	US-09-688-307A-1	Sequence 1, Appl

28	31.4	7.1	3785	1	US-08-485-618-98	Sequence 98, Appl
29	31.4	7.1	3785	1	US-08-605-672-98	Sequence 98, Appl
30	31.4	7.1	3785	2	US-08-482-293A-98	Sequence 98, Appl
31	31.4	7.1	3785	2	US-08-943-363-98	Sequence 98, Appl
32	31.4	7.1	3785	4	US-09-193-043-98	Sequence 98, Appl
33	31.4	7.1	3785	4	US-09-688-307A-98	Sequence 98, Appl
34	31.4	7.1	3956	1	US-08-485-618-97	Sequence 97, Appl
35	31.4	7.1	3956	1	US-08-605-672-97	Sequence 97, Appl
36	31.4	7.1	3956	2	US-08-482-293A-97	Sequence 97, Appl
37	31.4	7.1	3956	2	US-08-943-363-97	Sequence 97, Appl
38	31.4	7.1	3956	4	US-09-193-043-97	Sequence 97, Appl
39	31.4	7.1	3956	4	US-09-688-307A-97	Sequence 97, Appl
40	31	7.0	4371	4	US-09-462-136-8	Sequence 8, Appl
41	31	7.0	11459	4	US-09-462-136-7	Sequence 7, Appl
42	30	6.8	1035	4	US-09-457-066-6	Sequence 6, Appl
43	30	6.8	1773	4	US-09-134-001C-1553	Sequence 1553, Ap
44	29.8	6.7	1408	3	US-08-889-841B-22	Sequence 22, Appl
45	29.8	6.7	1497	2	US-07-916-098A-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-07-798-223A-1  
Sequence 1, Appl  
Patent No. 5422108  
GENERAL INFORMATION:  
APPLICANT: Mitkov, T. Erik  
APPLICANT: Filzmaurice, Leona Claire  
TITLE OF INVENTION: Protection of Plants Against Pathogens  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/798, 223A  
FILING DATE: 19911125  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/762, 679  
FILING DATE: 19-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 51984  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
TELEFAX: (619)552-0095  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 964 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 25..459  
US-07-798-223A-1  
Query Match 98.9%; Score 439; DB 1; Length 964;  
Best Local Similarity 100.0%; Pred. No. 1.5e-133; Indels 0; Gaps 0;  
Matches 439; Conservative 0; Mismatches 0;

OY	6	GGCGTCGTAAATCTGGGGTTCTCTCCCTTCGTGCGTCGCCAAGGCAAGGCTTTGA	65
Db	24	GGCTCTGTTATTTCTGGGTTCTCTCTCTCTCTGCTGTCCAAAGCAAGTCTTGA	83
OY	66	GAGATGTGACCTTGGCCAGACTCTGAAGAACTTGAGCTGACGGCTTTAAGGAGTCAG	129
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Db	144	CGTGGCAAACTGGTCTGTGTTGACCAAAATGGGAAGCAAGTATTAACACAAAAGCTACAAA	203
OY	186	CTACAATCCTAGACAGTGAAGACACGATTTATGGATATTTCAGATCAACACAGCAATGGTG	245
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OY	246	GTTGTAATGATGGCAAAACCCCTTAATGACAGTTGACGGCTGTCAATGATCTCGACGAAAT	305
Db	264	GTTGTAATGATGGCAAAACCCCTTAATGACAGTTGACGGCTGTCAATGATCTCGACGAAAT	323
OY	306	AATGAAAAATGACATGCTTAAAGCTGTAGCGGTGTCGAAGCATTTGTGCAAGTGACGAAG	365
Db	324	AATGAAAAATGACATGCTTAAAGCTGTAGCGGTGTCGAAGCATTTGTGCAAGTGACGAAG	383
OY	366	CATTACAGCCTGGGTGGCGATGGAAGAAAGTCATTGTTCGAGACCATGACGTCAGCACTTACGT	425
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OY	426	TGAGGGTTGCACCCCTGTA	444
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RESULT 2
US-09-385-982-344
: Sequence 344, Application US/09385982
: Patent No. 6262334
: GENERAL INFORMATION:
: APPLICANT: ENDEGE, WILSON O., ET AL.
: TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
: TITLE OF INVENTION: PRODUCTS: 11
: FILE REFERENCE: CCDNA-260XX
: CURRENT APPLICATION NUMBER: US/09/385,982
: CURRENT FILING DATE: 1999-08-30
: EARLIER APPLICATION NUMBER: 09/328,111
: EARLIER FILING DATE: 1999-06-08
: EARLIER APPLICATION NUMBER: 60/117,393
: EARLIER FILING DATE: 1999-01-27
: EARLIER APPLICATION NUMBER: 60/098,639
: EARLIER FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 544
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 344
: LENGTH: 657
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(657)
: OTHER INFORMATION: n = A,T,C or G
: US-09-385-982-344

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Query Match	56.3%	Score 250	DB 4	Length 657
Best Local Similarity	75.9%	Pred. No. 5.2e-72		
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			Gaps	1
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Db	75	AGTTGGCCAAACAACTGTGAAAAGATTTGGGAATGGATGGCTGACAGGGGAATCAGCTTAGCAA	134
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Db	135	ACTGGATGTGTTTGGCCAAATGGGAGAGGTTCACACACAGAGCTACAAACATCACAATG	194
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QY	429	GGGT 432	
Db	435	NGGT 438	

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RESULT 3
5182195-1
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO; KAISHO, YOSHIHIKO; YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:1:
; LENGTH: 394
5182195-1

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Query Match	35.4%	Score 157.2	DB 6	Length 394
Best Local Similarity	64.8%	Pred. No. 7.3e-42		
Matches 250	Conservative 0	Mismatches 133	Indels 3	Gaps 1
QY	62	TTGAGAGATGTAGCTTGCCAGAACTGTGAAGAACTTGGACCTGACGGCTATTAAGGAG	121	
DB	1	TCGAGAGATGCCAATTAGCCAGAACTTGAAGAGATTGGATGGATGACGGCTACCGTGA	60	
QY	122	TCAGCCTGGCAAACTGGCTTGTTGTTGACCAAAATGGGAAAGCAGTATTAACAAAAAGCTA	181	
DB	61	TTTCTTTACCCACAGCTGAGATGTCTTGCTGAATGGGAAATCCGGCTATTAACATAGAGCTA	120	
QY	182	CAAACTCAACATCTTAGCAGATGAAGACATGTATTAATGGATATTTACAGATCAACAGCAAAAT	241	
DB	121	CCAAATTACAAAGCCTGGCAGCGTCTCTACAGACTATGTGATTTTCCAAATTAACCTCTGAT	180	
QY	242	GGTGGTGTATGATGGCAAAACCCCTAATGCACTTGAACGGCTGCATGATCTCTGACGG	301	
DB	181	ATTGGTGTAAACATGGCAAGACTCCAGAGTCCGCTCAACGCCCTGCATTAATCTTGGCTCAG	240	
QY	302	AATTAATGSAAAATGACATGCTCTAAGCGTGAAGCGTGTGAAGGCATATTGTACAGCA--	359	
DB	241	CTTTGCTTCAGACACAACTGCTGATGTGTGTGCTGCTCGTAAAGAGAGTGTCCGTGACC	300	
QY	360	-GCAAGGCATTTACAGCCTGGCTGGCATATGAAATGCAATTTCTGACAGACCATGACCTAGCA	418	
DB	301	CACAGGGATTTAGACCTCGGGTCGGTGTGGAGAAACAGATGCCAAATTAAGAGATGTACAGC	360	
QY	419	GTTAGCTTAGGGTTGCACCTGTAA	444	
DB	361	AATAGTTCAAAGTTGTGTGTTTAA	386	







TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZpT-Fls  
US-08-232-463-14

Query Match 9.7%; Score 43; DB 1; Length 7218;  
Best Local Similarity 5.0%; Pred. No. 0.0005;  
Matches 19; Conservative 202; Mismatches 162; Indels 0; Gaps 0;

QY 49 CAAGGCAAGCTTTGAGATGTGACCTGCCAGACTGTGAAGAACTTGACCTGGAC 108  
DB 1471 CTATGCAAGTAAAGATGAAGAAATTTGCTACRRRRRRRRRRRRRRRRRR 1412  
QY 109 GGTATAGGAGCTGACCTGCGCAAACTGGTTGTGTGACCAATGGGAACAGTTAT 168  
DB 1411 RRR 1352  
QY 169 AACACAAAGCTCAAACTCAATCTAGCAGTGAAGACACTGATTATGGATTTTCA 228  
DB 1351 RRR 1292  
QY 229 ATCAACAGCAATGTGTGTATGATGCAAAACCCCTAATGACAGTTGCGCTGCT 288  
DB 1291 RRR 1232  
QY 289 GTATCTGCGCAATTAATGAAATGACATGCTAAGCTGTAAGCTGTGCAAGCAT 348  
DB 1231 RRR 1172  
QY 349 ATGTGAGTGAAGCATTAACGCTGGGTGTCATGGAAGTATGTGACGACCAT 408  
DB 1171 RRR 1112  
QY 409 GAGCTGACGAGTACGTTGAGG 431  
DB 1111 RRR 1089

RESULT 11  
US-08-385-590A-1  
Sequence 1, Application US/08385590A  
Patent No. 5824861  
GENERAL INFORMATION:  
APPLICANT: Aldwinckle, Herbert S.  
APPLICANT: No. 5824861e11, John L.  
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/385,590A  
FILING DATE: 08-FEB-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,347

FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/143  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-385-590A-1

Query Match 9.3%; Score 41.2; DB 1; Length 396;  
Best Local Similarity 48.1%; Pred. No. 0.00048;  
Matches 152; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

QY 89 TGAAGAACTTGACTGACGCTATTAAGGAGTCAGCTGCAAACTGTTGTGTTGA 148  
DB 59 TCAGAGAGCTTAGGAGAGAGGCTTCGATGAACCTTGATGATACTGGCTGCTTG 118  
QY 149 CCAATGGGAAGCAGTTATTAACACAAAGTACAAATACATCTAGCGTGAAGCA 208  
DB 119 TCGAAGACGAAGCGGAGGCTTTACCGATTAATCGTAAGCTTACAGAGGATCTC 178  
QY 209 CTGATTATGGATTAATTCAGATCAACAGCAATGCTGTATGATGCAAAACCCCTA 268  
DB 179 GAGACTAGGCGCTTCCAGATCAATGACAAATCTGTGAGTAAGGATCACTCT 237  
QY 269 AAGCATTTAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 328  
DB 238 -----GGAAGGATGCAAGCTGATGATGATGATGATGATGATGATGATGATG 292  
QY 329 CTGATGCTGTCGCAAGCATTAATGTCAGTGAAGCATTAACGCTGGGTGTCATGA 388  
DB 293 CAGCTACGTGGCGGCAAGAAATTACAAACCCCAAGTTGAGCGTTGACGATGGA 352  
QY 389 AAGCATTTGTCGAGA 404  
DB 353 AAAATCACTGTCAACA 368

RESULT 12  
US-09-021-520-1  
Sequence 1, Application US/09021520  
Patent No. 6100453  
GENERAL INFORMATION:  
APPLICANT: Aldwinckle, Herbert S.  
APPLICANT: No. 6100453e11, John L.  
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,520  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,590  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/143  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-09-021-520-1

Query Match 9.3%; Score 41.2; DB 3; Length 396;  
Best Local Similarity 48.1%; Pred. No. 0.0048;  
Matches 152; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

QY 89 TGAAGAACTTGGAGTGGAGCGCTTAAAGGAGTACGCTGGCAAACTGGTTGTTGA 148  
DB 59 TGCAGAGCTTGAAGAGAGAGAGCTTGAATGAATCTTGTAGTGAATGAGGCTGCTTG 118  
QY 149 CCAATGGGAAAGAGTATATAACAAAGCTTACAACTACAACTCTAGCGTGAAGCA 208  
DB 119 TCGAAGACGAAAGCGGAGGCTTTACCGTAAATGGTAAAGTTACAGAACGATCTC 178  
QY 209 CTGATTATGGATATTTGATGATCAACAGCAAAATGGTGGTAAATGAGCAAAACCCCTA 268  
DB 179 GAGACTAGGCGCTCTCCAGATCAATGACAAATATGTTGAGTAGAGGATCCACTCT 237  
QY 269 ATGAGTGGAGCGCTGATGATCTGACGCGAATTAAGAAATACATCGCTAAAG 328  
DB 238 -----GGAAGAGTTGCAACGCTGATCTGATCTACCTGACGACATTTAGCGTGG 292  
QY 329 CTGATGCTGTGCAAGCATATTTGAGTGAAGCAAGGATTAACGCTGGGGGAGTGA 388  
DB 293 CAGCTACGCTGGCGGAGAAAGATTTCAAACGCCACAAATTTGACGCTTGGTAGGATGGA 352  
QY 389 AAAGTATTTGCGAGA 404  
DB 353 AAAATCACTGTCACCA 368

## RESULT 13

US-08-449-644-3/C  
Sequence 3, Application US/08449644  
Patent No. 5856162  
GENERAL INFORMATION:  
APPLICANT: Schlessinger, Joseph  
APPLICANT: Sap, Jan M.  
APPLICANT: Ullrich, Axel  
APPLICANT: Vogel, Wolfgang  
APPLICANT: Fuchs, Miriam  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,644  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/087,244  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-042  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4374 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4371  
US-08-449-644-3

Query Match 7.3%; Score 32.2; DB 2; Length 4374;  
Best Local Similarity 45.5%; Pred. No. 1.3; Indels 138; Gaps 0;  
Matches 115; Conservative 0; Mismatches 138; Indels 138; Gaps 0;

QY 89 TGAAGAACTTGGAGTGGAGCGCTTAAAGGAGTACGCTGGCAAACTGGTTGTTGA 148  
DB 3569 TGAAGAGAGTGAAGTCTAGAGTGTATGCAATCATATCAAAATATGAGCTTAAATTC 3510  
QY 149 CCAATGGGAAAGAGCTTAAACAGCAAAAGCTTACAACTCAATCTAGCAGTGAAGCA 208  
DB 3509 CACACAGGAGTGGAGAGTCTTCCACATTAAGCAGGCTTAAATGGCATCATGATAAATA 3450  
QY 209 CTGATTATGGATATTTGATGATCAACAGCAAAATGGTGGTAAATGAGCAAAACCCCTA 268  
DB 3449 ATGACTGTTCTCTGCTGCTGATCAATTTAATGCGCGAGATGTAAAGCTTTCACACAG 3390  
QY 269 ATGAGTGGAGCGCTGATGATCTGACGCGAATTAAGAAATGAGATGCGTAAAG 328  
DB 3389 TTGTAGATGTCAACACACACCTCTCTTACGACATGTCAGCATTTAGTCAATTAACAAATG 3330  
QY 329 CTGAGCGTGTGC 341  
DB 3329 TAAACAGCCTGTGC 3317

## RESULT 14

US-08-087-244A-3/C  
Sequence 3, Application US/08087244A  
Patent No. 5863755  
GENERAL INFORMATION:  
APPLICANT: Schlessinger, Joseph  
APPLICANT: Sap, Jan M.  
APPLICANT: Ullrich, Axel  
APPLICANT: Vogel, Wolfgang  
APPLICANT: Fuchs, Miriam  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk





Db 181 ACAAACTACATCTTACAGTGAAGACATGATTATGATATTCAGATCAACAGCAAA 240  
QY 241 TGGTGTGTAATGATGAGCAAAACCCCTAATGATGAGCGTGTATGATCTGACG 300  
Db 241 TGGTGTGTAATGATGAGCAAAACCCCTAATGATGAGCGTGTATGATCTGACG 300  
QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAGCATATTTGACGTAG 360  
Db 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAGCATATTTGACGTAG 360  
QY 361 CAAGGCAATACAGCGTGGGTGCGATGGAAGATGATTTGTCGAGACATGACGTACAGT 420  
Db 361 CAAGGCAATACAGCGTGGGTGCGATGGAAGATGATTTGTCGAGACATGACGTACAGT 420  
QY 421 TACGTTGAGGGTGTGACACCTGTAA 444  
Db 421 TACGTTGAGGGTGTGACACCTGTAA 444

RESULT 2  
US-09-978-199-3  
; Sequence 3, Application US/09978199  
; Patent No. US20020104126A1  
; GENERAL INFORMATION:  
; APPLICANT: FOSBE, GREGORY P.  
; APPLICANT: VELICHKO, SHARLENE  
; TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS  
; FILE REFERENCE: 42202  
; CURRENT APPLICATION NUMBER: US/09/978,199  
; PRIOR FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: 60/240,967  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 10132  
; TYPE: DNA  
; ORGANISM: Bovine sp.  
US-09-978-199-3

Query Match 100.0%; Score 444; DB 10; Length 10132;  
Best local Similarity 100.0%; Pred. No. 4,1e-133;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTCGTATATCTGAGGTTCTCTTCTGCTGCTGCCAAGCAAGTGC 60  
Db 5767 ATGAAGGCTCTCGTATATCTGAGGTTCTCTTCTGCTGCTGCCAAGCAAGTGC 5826  
QY 61 TTTGAGAGATGTGAGCTTCCAGAACTCTGGAAGAACTTGGACGTGACGGCTATAAGGGA 120  
Db 5827 TTTGAGAGATGTGAGCTTCCAGAACTCTGGAAGAACTTGGACGTGACGGCTATAAGGGA 5886  
QY 121 GTCAGCCTGGCAAACTGTTGTGTTGACCAATGGGAAGCAGTTATTAACCAAAAGCT 180  
Db 5887 GTCAGCCTGGCAAACTGTTGTGTTGACCAATGGGAAGCAGTTATTAACCAAAAGCT 5946  
QY 181 ACAAACTACAATCTCTAGCAGTGAAGCACTGATTTATGGAATATTTTCAGATCAACAGCAA 240  
Db 5947 ACAAACTACAATCTCTAGCAGTGAAGCACTGATTTATGGAATATTTTCAGATCAACAGCAA 6006  
QY 241 TGGTGTGTAATGATGAGCAAAACCCCTAATGATGAGCGTGTATGATCTGACGACG 300  
Db 6007 TGGTGTGTAATGATGAGCAAAACCCCTAATGATGAGCGTGTATGATCTGACGACG 6066  
QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAGCATATTTGACGTAG 360  
Db 6067 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAGCATATTTGACGTAG 6126  
QY 361 CAAGGCAATACAGCGTGGGTGCGATGGAAGATGATTTGTCGAGACATGACGTACAGT 420  
Db 6127 CAAGGCAATACAGCGTGGGTGCGATGGAAGATGATTTGTCGAGACATGACGTACAGT 6186  
QY 421 TACGTTGAGGGTGTGACACCTGTAA 444

Db 6187 TACGTTGAGGGTGTGACACCTGTAA 6210

RESULT 3  
US-09-969-347-318  
; Sequence 318, Application US/09969347  
; Patent No. US20020115085A1  
; GENERAL INFORMATION:  
; APPLICANT: Eder, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign  
; FILE REFERENCE: 689290-69  
; CURRENT APPLICATION NUMBER: US/09/969,347  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,598  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: US/60/237,604  
; NUMBER OF SEQ ID NOS: 318  
; SOFTWARE: Patentln version 3.0  
; SEQ ID NO 318  
; LENGTH: 748  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-969-347-318

Query Match 52.8%; Score 279; DB 10; Length 748;  
Best local Similarity 78.1%; Pred. No. 3.5e-80;  
Matches 349; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 ATGAAGGCTCTCGTATATCTGAGGTTCTCTTCTGCTGCTGCCAAGCAAGTGC 60  
Db 14 ATGAAGGCTCTCATTTGTTCTGAGGCTTCTCTTCTGCTGCTGCCAAGCAAGTGC 73  
QY 61 TTTGAGAGATGTGACCTTGCAGAACTCTGGAAGAACTTGGACGTGACGGCTATTAAGGGA 120  
Db 74 TTTGAGAGATGTGAGTGTGAGTGGCCAGAACTCTGGAAGAACTTGGACGTGACGGCTATTAAGGGA 133  
QY 121 GTCAGCCTGGCAAACTGTTGTGTTGACCAATGGGAAGCACTTATTAACCAAAAGCT 180  
Db 134 ATGAGCCTGAGCAAACTGATGTTGTTGCAAAATGGGAGAGTGTTCACACACGAGCT 193  
QY 181 ACAAACTACAATCTCTAGCAGTGAAGCACTGATTTATGGAATATTTTCAGATCAACAGCAA 240  
Db 194 ACAAACTACAATCTCTAGCAGTGAAGCACTGATTTATGGAATATTTTCAGATCAATAGCCG 253  
QY 241 TGGTGTGTAATGATGAGCAAAACCCCTAATGATGAGCGTGTATGATCTGACGACG 300  
Db 254 TACGTTGTAATGATGAGCAAAACCCCAAGGACAGTATGATGCTGATTTATCTGACGAGT 313  
QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAGCATATTTGACGTAG 359  
Db 314 GCTTTGCTGCAAGATTAACATGCTGATGCTGATGCTGCTGCAAGAGAGGTTGCTGAT 373  
QY 360 --GCAAGCATTACAGCCTGGGTGCGATGGAAGATGATTTGTCGAGACATGACGTACG 417  
Db 374 CCACAGGCAATTAAGAGATGAGTGGTGGCATGGAAGATGTTGCAAAACAGAGATGTCCT 433  
QY 418 AGTTAGCTTGAAGGTTGACACCTGTAA 444  
Db 434 CAGTATGTTCAAGGTTGAGAGTAA 460

RESULT 4  
US-10-046-935-1085  
; Sequence 1085, Application US/10046935  
; Patent No. US20020156011A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Wang, Aljun

```

Query Match      60.3%; Score 267.8; DB 9; Length 478
US-09-878-178-1085
; Result 5
; Sequence 1065, Application US/09878178
; Patent No. US2002017552A1
; GENERAL INFORMATION:
; APPLICANT: JIANG, YUGU
; APPLICANT: HARLOCKER, SUSAN L.
; APPLICANT: SECRET, HEATHER
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
; SEQ ID NO 1085
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-1085

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Query Match	60.3%;	Score 267.8;	DB 9;	Length 478;
Best Local Similarity	78.0%;	Pred. No. 1.2e-76;		
Matches 336;	Conservative 0;	Mismatches 92;	Indels 3;	Gaps 1;

QY 1 TTTGGGGTTTCTTCCTTTCTGTGTCGCTGCACAGCGAAGCTTTGAGAGATGAGG 76  
Db 2 TTTGGGGCTTTGTCTCTCTTTCTGTGTACGGTCCAGCGCAAGCTTTTGAAGGTGTAGT 61  
QY 77 TTGCGCAAGACTGTGAAGAACTTGGACTGTGACGGCTATATAGGAGTCAAGCCTGGCAAACT 136  
Db 62 TTGCGCAAGACTGTGAAGAACTTGGGAAATGGATGGCTATACAGGGGAATCAAGCCTGAGCAAACT 121  
QY 137 GGTGTGTGTGACCAATGGGAAGCAGTTATATACACAAAGCTACAACTATACATCTTA 196

Db	122	GGATGTGTTGGCCAAATGGAGAGTGGTTACACACACAGCATCAAACTACATCTG	181
QY	197	GCAGTGAAGCACTGATTATGGGATATTTACAGTACACAGAAATGGTGGTATATG	256
Db	182	GAGACAGAAAGCACTGATTATGGGATATTTCAATCAATCAAAAGCGGTACTGGTGATATG	241
QY	257	GCAAAACCCCTAATGCAGTTGACGGCTGTCATGATCTCCGACGAAATTAATGAAATG	316
Db	242	GCAAAACCCGAGGACAGTTAATGGCTGTCATTATCTCGAGTGCCTTGGTCGAAATA	301
QY	317	ACATGCCCTAAAGCTGTAGCGTGTGCAAAAGCATATTTGTAGTGA---GCAAGCATTAAG	373
Db	302	ACATCCCTATGCTGTGATGGTTGTGGCAAAAGGGTTGTCGAGATCCACAAGGCATTGAG	351
QY	374	CCAGGGTGGCATGGAAGAAATCATTTCTCAGACATGATGCGTACAGATTAAGTTAGAGTT	433
Db	362	CATGGGTGGCATGGAAGAAATCTTTCCAAACAGAGATGTCCGTACATATGTTCAAGTT	421
QY	434	GCACCTGTAA 444	
Db	422	GTGGAGTGTAA 432	

```

RESULT 7
US-10-001-873-11
: Sequence 11, Application US/10001873
: Patent No. US20020160388A1
: GENERAL INFORMATION:
: APPLICANT: Macina, Roberto
: APPLICANT: Reclapon, Hervé
: APPLICANT: Chen, Sei-Yu
: APPLICANT: Sun, Yongming
: APPLICANT: Liu, Yonghua
: APPLICANT: Turner, Leah
: TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
: FILE REFERENCE: DEX-0275
: CURRENT APPLICATION NUMBER: US/10/001,873
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/252,055
: PRIOR FILING DATE: 2000-11-20
: PRIOR APPLICATION NUMBER: 60/252,496
: PRIOR FILING DATE: 2000-11-22
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 11
: LENGTH: 2467
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (2319)..(2319)
: OTHER INFORMATION: a, c, g or t
: US-10-001-873-11

```

	Query Match	59.7%	Score 265.2	DB 9	Length 2467
	Best Local Similarity	78.1%	Pred. No. 2.1e-75		
	Matches 345	Conservative 0	Mismatches 93	Indels 4	Gaps 2
QY	6	GGCTCTGTTATCTGGGGTTCTCTTCCTTCCTTCGTGCTGCTCCAGGCAAGGCTTTGA	65		
Db	1	GGCTCTCATGTTGTGGGGCTTGTCCTTCCTTCGTATACGCTCC-AGGCAAGCTTTGA	59		
QY	66	GAGATGTAGCTTGGCCAACTCTGAAAGAACTTGGACTGGAGCGCTATTAAGGACTCAG	125		
Db	60	AAGGTGTGTTGGCCCAACACTCTGAAAAGTTTGGATGTGATGGCTACAGGGGAATCAG	119		
QY	126	CCTGGCAACTGGTGTGTTTGACCAATGGGAAGACAGTTATACACAAACCTACTCAA	185		
Db	120	CCAGCAAACTGGATGTTGTTGGCCAAATGGGAAAGTGTTACACACAGAGCTCAAA	179		
QY	186	CTACAACTCTAGCACTGAAGCACTGATTATGGATATTTTCAGATCAACAGCAATGGTG	245		
	180	CTACAACTGTGGAGACAGCAAGCACTGATTATGGGATTTTCAGATCAATAGCCGCTACAG	239		

QY	246	GTTGAATGATGGCGAAACCCCTTAATGCACTTACGGGTGATGATGATCTCCAGCAAGTT	305
Db	240	GTTGAATGATGGCGAAACCCCGAGGACCTTAATGCTGTCTCATTTTATCTGCACTGCTTT	299
QY	306	AATGGAATAATGACATGCTTAAAGCTGTACCGTGTGCCAAGCATATTGTCACTGA ---GCA	362
Db	300	GTTCGAAGATTAACATGCTGTATGCTGTAGCTTGTGCCAAGAAGGGTTGTCCGTGATCCACA	355
QY	363	AGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTGAGACCATGACGTACAGCACTTA	422
Db	360	AGGCATTAGAGCATGGGTGGCATGGAGAATCGTTCAAAACAGAGATGTCCTCAGTA	419
QY	423	CGTTGAGGGTGGCAACCTGTAA	444
Db	420	TGTTCAAGGTTGTGAGTGTAA	441

```

RESULT 8
US-09-871-161-344
: Sequence 344, Application US/09871161
: Publication No. US20030097666A1
: GENERAL INFORMATION:
: APPLICANT: ENDEGE, WILSON O., ET AL.
: TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
: TITLE OF INVENTION: PRODUCTS: II
: FILE REFERENCE: CCDNA-260XX
: CURRENT APPLICATION NUMBER: US/09/871,161
: CURRENT FILING DATE: 2001-05-31
: PRIOR APPLICATION NUMBER: 09/328,111
: PRIOR FILING DATE: 1999-06-08
: PRIOR APPLICATION NUMBER: 60/117,393
: PRIOR FILING DATE: 1999-01-27
: PRIOR APPLICATION NUMBER: 60/098,639
: PRIOR FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 544
: SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
: SEQ ID NO 344
: LENGTH: 657
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(657)
: OTHER INFORMATION: n = A,T,C or G
: US-09-871-161-344

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Db 315 ATACATGCTGATCTGTAGCTTGTGCAGAAAANGTTGTCCCGATGCACAGGCATT 374  
OY 369 TACAGCTGGTGGATGAGAAAGCATTTGTGACACATGACGTCAGCATTTAGCTTGA 428  
Db 375 AAGACATGGGTGGATGAGAAATGTTGTTCACAAACAGATGTCCGACATGTCTCA 434  
OY 429 GGGT 432  
Db 435 NGGT 438

## RESULT 9

US-10-060-036-2544/C  
; Sequence 2544, Application US/10060036  
; Publication No. US20030073144A1

## GENERAL INFORMATION:

APPLICANT: Benson, Darin R.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Persing, David H.  
APPLICANT: Hepler, William T.

APPLICANT: Jiang, Yugu

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.566

CURRENT APPLICATION NUMBER: US/10/060,036

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2544

LENGTH: 606

TYPE: DNA

ORGANISM: Homo sapiens

NAME/KEY: misc\_feature

LOCATION: 603

OTHER INFORMATION: n = A,T,C or G

US-10-060-036-2544

## Query Match

Best Local Similarity 42.8%; Score 190; DB 9; Length 606;  
Matches 259; Conservative 0; Mismatches 76; Indels 4; Gaps 2;

OY 109 GGCTATAGGAGTGCACCTGGCAAACTGTTGTGTTGACCAATGGGAAGCATTTAT 168  
Db 605 GGTTACAGGGAGATCAGCTTACCAATCTGATGTGTTTCCCAAT-GGAGAGTGTAC 547  
OY 169 AACACAAAAGCTACAACTACATCTAGCAGTGAAGCATGATTATGGATTATTCAG 228  
Db 546 AACACAGAGCTACAACTACATCTGAGACAGACATGATTATGGATTATTCAG 487  
OY 229 ATCAACAGCAATGGGTGTGTAATGATGCAAAACCCCTAATGACGTTACGGCTGAT 288  
Db 486 ATCAATAGCCGTACGCTGTAATGTCAAAACCCCGAGGAGATTATGCTGTCAAT 427  
OY 289 GATCTCGAGCAATTAATGAAATGACATCGCTAAGCTGTAGCGTGCACCAAGCAT 348  
Db 426 TATCTCGAGTGTCTTGTGTCAGATACATCGCTGATGCTGTACCTGTGCAAGAG 367  
OY 349 ATTGTAGTGA--GCAAGCATTACAGCTGGTGGCATGAAAAAGCATTTGTGAGAC 405  
Db 366 GTTGTCCGTGATCCACAGCATTTAGACATGGGTGGCATGGAATGTTGTCAAAAC 307  
OY 406 CATGAGTCAAGCATTTAGCTGTGAGGTTGCACCTGTAA 444  
Db 306 AGAGATGCTCGTACATATGTTCAAGGTTGTGAGGTGTA 268

RESULT 10  
US-10-046-935-1606/C  
; Sequence 1606, Application US/10046935  
; Patent No. US20020156011A1  
; GENERAL INFORMATION:

APPLICANT: Jiang, Yugu  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Secrist, Heather  
APPLICANT: Wang, Aijun  
APPLICANT: Stoik, Tom A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.527C1  
CURRENT APPLICATION NUMBER: US/10/046,935  
CURRENT FILING DATE: 2002-01-15  
NUMBER OF SEQ ID NOS: 2239  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1606  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-046-935-1606

## Query Match

Best Local Similarity 41.8%; Score 185.4; DB 9; Length 582;  
Matches 241; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

OY 133 AACTGTTGTTTGGACCAATGGGAAGCATTTATACACAAAGCTACAACTACAT 192  
Db 582 AACTGATGTGTTGGCCCAATGGAGAGTGTTCACACACAGCATACAACTACAT 523  
OY 193 CCTGACAGTGAACACATGATTATGGATATTTCAGATCAACAGCAATGATGAT 252  
Db 522 CTTGAGACAGACACATGATTATGGATATTTCAGATCAACAGCATGATGAT 463  
OY 253 GATGCAAAACCCCTAATGACGCTGTGATGATGATGATGATGATGATGATGAT 312  
Db 462 GATGCAAAACCCAGAGAGCATTAAGCTGATGATGATGATGATGATGATGAT 403  
OY 313 AATGATCGCTAAGCTGTGAGCTGTGCAAAAGCATATGTCAGTGA--GCAAGCAT 369  
Db 402 GATAACATCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 343  
OY 370 ACAGCTGGTGGCATGGAAGATGATGATGATGATGATGATGATGATGATGATGAT 429  
Db 342 AGAGATGGTGGCATGGAAGATGATGATGATGATGATGATGATGATGATGATGAT 283  
OY 430 GATTGACCTGTGA 444  
Db 282 GATTGAGATGTA 268

## RESULT 11

US-09-878-178-1606/C  
; Sequence 1606, Application US/09878178  
; Patent No. US20020177552A1

## GENERAL INFORMATION:

APPLICANT: Jiang, Yugu

APPLICANT: Harlocker, Susan L.

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.527

CURRENT APPLICATION NUMBER: US/09/878,178

NUMBER OF SEQ ID NOS: 2237

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1606

LENGTH: 582

TYPE: DNA

ORGANISM: Homo sapien

US-09-878-178-1606

Query Match  
Best Local Similarity 41.8%; Score 185.4; DB 9; Length 582;  
Matches 241; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

OY 133 AACTGTTGTTTGGACCAATGGGAAGCATTTATACACAAAGCTACAACTACAT 192

Db 582 AACTGATGTGTTGGCAAAATGAGAGTGTGTACAAACAGACGACTACAAATGCAT 523  
QY 193 CCAAGCAGTAAGCACTGATTTATGGATTTTCACATCAACAGCAAAATGGTGTAA 252  
Db 522 GCTGGAGACAGAAAGCATGATTTATGGATTTTCACATCAAAATGGTGTAA 463  
QY 253 GATGGCAAAACCCCTAATGAGTGTGAGCGCTGATGATTCCTGACAGCAATTAAGAA 312  
Db 462 GATGGCAAAACCCAGAGAGAGTAAATGCTGATTTATCTGACAGTGTGCTGCA 403  
QY 313 AATGACATGCTAAAGCTGTAGCGGTGCAAAACATATTGTCACTGA---GCAAGCATT 369  
Db 402 GATACATGCTGATGCTGTAGCTGTGCAAAAGAGGTGTGCTGATCACAAGCATT 343  
QY 370 ACAGCGTGGTGGCAGTGAAGTCAATGTCGAGACCAAGACAGTCAAGCATTGAG 429  
Db 342 AGAGCATGGTGGCAGTGAAGTCAATGTCGAGACCAAGAGATGCTGATGATGTTCA 283  
QY 430 GGTGGACCCCTGTAA 444  
Db 282 GGTGGAGAGTGTAA 268

RESULT 12  
US-10-146-502-1606/c  
Sequence 1606, Application US/10146502  
Publication No. US20030069180A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugu  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Secrist, Heather  
APPLICANT: Wang, Aijun  
APPLICANT: Stolk, John A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.52762  
CURRENT APPLICATION NUMBER: US/10/146,502  
CURRENT FILING DATE: 2002-05-14  
NUMBER OF SEQ ID NOS: 2241  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1606  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-146-502-1606

Query Match 41.8%; Score 185.4; DB 9; Length 582;  
Best Local Similarity 76.5%; Pred. No. 7.4e-50;  
Matches 241; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 133 AACTGTTGTGTTGACCAAAATGGGAAAGCACTTAATCAACAAAGCTACAACTACAT 192  
Db 582 AACTGATGTGTTGGCAAAATGAGAGTGTGTACAAACAGCAAAATGGTGTAA 523  
QY 193 CCTAGCAGTAAGCACTGATTTATGGATTTTCACATCAACAGCAAAATGGTGTAA 252  
Db 522 GCTGGAGACAGAAAGCATGATTTATGGATTTTCACATCAAAATGGTGTAA 463  
QY 253 GATGGCAAAACCCCTAATGAGTGTGAGCGCTGATGATTCCTGACAGCAATTAAGAA 312  
Db 462 GATGGCAAAACCCAGAGAGAGTAAATGCTGATTTATCTGACAGTGTGCTGCA 403  
QY 313 AATGACATGCTAAAGCTGTAGCGGTGCAAAACATATTGTCACTGA---GCAAGCATT 369  
Db 402 GATACATGCTGATGCTGTAGCTGTGCAAAAGAGGTGTGCTGATCACAAGCATT 343  
QY 370 ACAGCGTGGTGGCAGTGAAGTCAATGTCGAGACCAAGACAGTCAAGCATTGAG 429  
Db 342 AGAGCATGGTGGCAGTGAAGTCAATGTCGAGACCAAGAGATGCTGATGATGTTCA 283  
QY 430 GGTGGACCCCTGTAA 444  
Db 282 GGTGGAGAGTGTAA 268

Db 282 GGTGGAGAGTGTAA 268

RESULT 13  
US-09-796-692-8055  
Sequence 8055, Application US/09796692  
Publication No. US20020198362A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER  
FILE REFERENCE: 2077.001200  
CURRENT APPLICATION NUMBER: US/09/796,692  
CURRENT FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: 60/223,378  
PRIOR FILING DATE: 2000-08-07  
NUMBER OF SEQ ID NOS: 9597  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8055  
LENGTH: 367  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (331)  
OTHER INFORMATION: n-A,T,C or G  
NAME/KEY: unsure  
LOCATION: (361)  
OTHER INFORMATION: n-A,T,C or G  
US-09-796-692-8055

Query Match 38.9%; Score 172.6; DB 9; Length 367;  
Best Local Similarity 75.9%; Pred. No. 8.1e-46;  
Matches 227; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 149 CCAATGGGAAAGCATTTATACCAAAAGCACTACAAATCTAGCAGTGAAGCA 208  
Db 1 CCAATGGGAGAGTGTGTACAAACAGCACTACAAATCTAGCAGTGAAGCA 60  
QY 209 CTGATTTAGGATTTTCACATCAACAGCAAAATGGTGTATGATGCAAAACCCCTA 268  
Db 61 CTGATTTAGGATTTTCACATCAACAGCAAAATGGTGTATGATGCAAAACCCCTA 120  
QY 269 ATGAGTTGAGCGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 328  
Db 121 GAGAGTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
QY 329 CTGAGCGTGTGCAAGCATTTATGTCAGTGA---GCAAGCATTTACAGCCTGGTGGCAT 385  
Db 121 GAGAGTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180

Db 181 CTGATCTGTGCAAGAGGCTTCCTGATCCACAGCATTAAGCATGGGTGGCAT 240  
QY 386 GGAAGATCATTTGCGAGACATGACCTGACAGTTACGTTGAGGTTGACCCCTGTA 444  
Db 241 GGAGAAATCGTTGCAAAACAGAGATGTCCTGATGTTCAGAGTTGTGGAGTGTAA 299

## RESULT 14

US-10-040-862-8055  
; Sequence 8055, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Galger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 8055  
; LENGTH: 367  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (331)  
; OTHER INFORMATION: n=A,T,C or G  
; NAME/KEY: unsure  
; LOCATION: (361)  
; OTHER INFORMATION: n=A,T,C or G  
US-10-040-862-8055

Query Match 38.9%; Score 172.6; DB 9; Length 367;  
Best Local Similarity 75.9%; Pred. No. 8.1e-46;

Matches 227; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 149 CCAATGGGAAAGCTTATTAACAAAGCTACAACTACATCTAGCAGTGAAGA 208  
Db 1 CCAATGGGAGAGTGTACAAACAGAGCTACAACTACATCTAGCAGTGAAGA 60  
QY 209 CTGATTAATGGGATATTTCAGATCAACAGCAAAATGTTGTGTATGATGCAAAACCCCTA 268

Db 61 CTTATTAATGGGATATTTCAGATCAATAGCCCTACTGGTGTATGATGCAAAACCCAG 120  
QY 269 ATGACGTTGAGCGCTGTCATGATATCTGACAGCAATTAATGAAATGACATCGTAAAG 328  
Db 121 GAGCACTTAATGGCTGTCTCATTTATCTCGAGTGTCTTGTGCAAGATACATCGCTGANG 180  
QY 329 CTGTAGCGTGTGCAAAAGCATATTGTCAGTGA---GCAAGCATTAACGCTGGTGGCAT 385  
Db 181 CTGTAGCTGTGTGCAAAAGAGGTTGTCCTGATCCACAAAGCATTTAGAGCATGGTGGCAT 240  
QY 386 GGAAGATCATTTGCGAGACATGACCTGACAGTTAGCTGAGGTTGACCCCTGTA 444  
Db 241 GGAGAAATCGTTGTCAAAACAGAGATGTCCTGATGTTCAGAGTTGTGAGTGTAA 299

## RESULT 15

US-10-102-524-791  
; Sequence 791, Application US/10102524  
; Publication No. US20030109434A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Galger, Alexander  
; APPLICANT: Gordon, Brian  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.572  
; CURRENT APPLICATION NUMBER: US/10/102,524  
; CURRENT FILING DATE: 2002-03-19  
; NUMBER OF SEQ ID NOS: 1863  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 791  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 447, 456, 466  
; OTHER INFORMATION: n = A,T,C or G  
US-10-102-524-791

Query Match 38.9%; Score 172.6; DB 9; Length 522;  
Best Local Similarity 75.9%; Pred. No. 9.9e-46;

Matches 227; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 149 CCAATGGGAAAGCTTATTAACAAAGCTACAACTACATCTAGCAGTGAAGA 208  
Db 1 CCAATGGGAGAGTGTTCACAAACAGAGCTACAACTACATCTAGCAGTGAAGA 60  
QY 209 CTGATTAATGGGATATTTCAGATCAACAGCAAAATGTTGTGTATGATGCAAAACCCCTA 268  
Db 61 CTTATTAATGGGATATTTCAGATCAATAGCCCTACTGGTGTATGATGCAAAACCCAG 120  
QY 269 ATGACGTTGAGCGCTGTCATGATATCTGACAGCAATTAATGAAATGACATCGTAAAG 328  
Db 121 GAGCACTTAATGGCTGTCTCATTTATCTCGAGTGTCTTGTGCAAGATACATCGCTGANG 180  
QY 329 CTGTAGCGTGTGCAAAAGCATATTGTCAGTGA---GCAAGCATTAACGCTGGTGGCAT 385  
Db 181 CTGTAGCTGTGTGCAAAAGAGGTTGTCCTGATCCACAAAGCATTTAGAGCATGGTGGCAT 240  
QY 386 GGAAGATCATTTGCGAGACATGACCTGACAGTTAGCTGAGGTTGACCCCTGTA 444  
Db 241 GGAGAAATCGTTGTCAAAACAGAGATGTCCTGATGTTCAGAGTTGTGAGTGTAA 299

Search completed: July 5, 2003, 06:16:09  
Job time: 133 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 06:13:53 ; Search time 1381 Seconds

(without alignments)  
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Title: US-09-978-199-1

Perfect score: 444  
Sequence: 1 atgaagctctcgtatctc.....ttgagggtgcaccctgttaa 444

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Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
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6: gb\_pat:\*  
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11: gb\_sts:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
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40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	444	100.0	459	6 108277	108277 Sequence 2
2	444	100.0	951	4 BOVL522B	M26243 Bovine lyso
3	444	100.0	1060	4 BOVL2YMW7A	L23758 Bos taurus
4	439	98.9	964	6 112256	M26245 Sequence 1
5	437	98.4	909	4 BOVL522A	M26241 Bovine lyso
6	437	98.4	963	6 109315	109315 Sequence 1
7	395	89.0	877	4 BOVL522C	M26244 Bovine lyso
8	310	69.8	786	4 BOVL522DA	M26240 Bovine lyso
9	202	45.5	1082	4 BOVL523A	M26242 Bovine lyso
10	165	37.2	10212	4 BOVL502MB	M50508 Bos taurus
11	130	29.3	8051	4 BOVL502MC	M50509 Bos taurus
12	96	21.6	881	4 SHPL2M1B	M2493 Sheep lysoz
13	96	21.6	881	4 SHPL2M1C	M2494 Sheep lysoz
14	96	21.6	881	4 SHPL2M2A	M2495 Sheep lysoz
15	94	21.2	891	4 SHPL2M1B	M26246 Bovine lyso
16	87	19.6	881	4 SHPL2M1A	M32492 Sheep lysoz
17	87	19.6	885	4 AXIL2M1	M32499 A. axis, lys
18	80	18.0	873	4 AXIL2M2	M32500 A. axis, lyso
19	76	17.1	906	4 BOVL521A	M26245 Bovine lyso
20	76	17.1	12222	4 BOVL502MA	M50509 Bos taurus
21	64	14.4	8943	4 BRU19466	U19466 Bos taurus
22	63	14.2	875	4 SHPL2M3A	M32496 Sheep lysoz
23	63	14.2	1522	4 BRU19469	U19469 Bos taurus
24	61	13.7	1248	4 BOVL2YMW14D	L23756 Bos taurus
25	59	13.3	495	4 OAL2A2	AR170553 Ovis arlie
26	56	12.6	2499	4 OAL2B1	AR170555 Ovis arlie
27	52	11.7	875	4 SHPL2M4A	M32497 Sheep lysoz
28	52	11.7	875	4 SHPL2M4B	M32498 Sheep lysoz
29	51	11.5	1990	4 OAL2A1	AR170552 Ovis arlie
30	49	11.0	3264	4 BRU19468	U19468 Bos taurus
31	46	10.4	1020	4 BOVL2YMW5A	L23757 Bos taurus
32	46	10.4	1529	4 BOVL502YM	U19980 Bos taurus
33	46	10.4	12039	4 BRU25810	U25810 Bos taurus
34	43	9.7	680	4 OAL2B2	AR170557 Ovis arlie
35	38	8.6	326	4 OAL2A3	AR170554 Ovis arlie
36	33	7.4	165	9 CAL2M2	U76935 Colobus arlie
37	33	7.4	447	9 CGU76916	U76916 Colobus que
38	32	7.2	165	9 PNLM2M2	U76942 Pygathrix n
39	32	7.2	165	9 NLIZM2	U76946 Nasalis lar
40	32	7.2	447	9 TCU76917	U76917 Trachypithe
41	32	7.2	447	9 TCU76918	U76918 Trachypithe
42	31	7.0	165	9 ANL2M2	U76950 Allenopithe
43	31	7.0	165	9 EPL2M2	U76957 Erythrocebu
44	31	7.0	165	9 MTL2M2	U76953 Miopithecus
45	31	7.0	447	9 CUU76923	U76923 Callithrix

#### ALIGNMENTS

RESULT 1  
LOCUS 108277 459 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 2 from Patent EP 0374913.  
ACCESSION 108277  
VERSION 108277.1 GI:589012  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 459)  
AUTHORS Digan, M.E.  
TITLE Pichia pastoris glyceroldehydro-3-phosphate dehydrogenase gene  
JOURNAL Patent: EP 0374913-A1 2 27-JUN-1990;  
FEATURES Location/Qualifiers

source	1..459	/organism="unknown"
BASE COUNT	132 a 89 c 119 g 119 t	
ORIGIN		
Query Match	100.0%; Score 444; DB 6; Length 459;	
Best Local Similarity	100.0%; Pred. No. 6,4e-249;	
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 ATGAAGCTCTGCTATTATCTGAGGGTTCCTCTCTCTGCTGCTGCCAAGCGAAGTGC 60	
DB		
OY	7 ATGAAGGCTCTGCTATTATCTGAGGGTTCCTCTCTCTGCTGCTGCCAAGCGAAGTGC 66	
OY	61 TTGAGACATGTGAGCTTGCCAGAACCTGTAAGAACTTGACACTGAGCGCTATTAAAGGA 120	
DB		
OY	121 GTCAGCCCTGGCAAACTGGTGTGTTGACCAAAATGGGAAGACAGTTATTACCAAAAGCT 180	
DB	127 GTCAGCCCTGGCAAACTGGTGTGTTGACCAAAATGGGAAGACAGTTATTACCAAAAGCT 186	
OY	181 ACAAACTCAATCTCCTAGCAGTGAAGACAGTATTAAGGATATTTGACATCAACAGCAAA 240	
DB	187 ACAAACTCAATCTCCTAGCAGTGAAGACAGTATTAAGGATATTTGACATCAACAGCAAA 246	
OY	241 TGGTGGTATTAATGATGGCAAAACCCCTAATGACAGTGAAGCGCTGCATGATATCCGCAAGC 300	
DB	247 TGGTGGTATTAATGATGGCAAAACCCCTAATGACAGTGAAGCGCTGCATGATATCCGCAAGC 306	
OY	301 GAATTAATGAAAAATGACATGCTAAGACCTGAGCGTGTGCAAAAGCATATTGTCAAGTGAAG 360	
DB	307 GAATTAATGAAAAATGACATGCTAAGACCTGAGCGTGTGCAAAAGCATATTGTCAAGTGAAG 366	
OY	361 CAAGCATATTAAGCGCTGGGTGGCATGCAAAAGTCAATTTGCAGACCATGACGTACAGCT 420	
DB	367 CAAGCATATTAAGCGCTGGGTGGCATGCAAAAGTCAATTTGCAGACCATGACGTACAGCT 426	
OY	421 TACGTTGAGGGTTGCACCCCTGTA 444	
DB	427 TACGTTGAGGGTTGCACCCCTGTA 450	
RESULT 2		
LOCUS	BOVL522B	951 bp mRNA linear MAM 27-APR-1993
DEFINITION	Bovine lysozyme c isozyme 2b mRNA, complete cds.	
ACCESSION	M26243.1	GI:163316
VERSION	M26243.1	GI:163316
KEYWORDS	lysozyme.	
SOURCE	Bovine abomasum, cDNA to mRNA, clone lambda-cBL[12,42].	
ORGANISM	Bos taurus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos. 1 (bases 1 to 951)	
AUTHORS	Ircin,D.M. and Wilson,A.C.	
TITLE	Multiple cDNA sequences and the evolution of bovine stomach lysozyme	
JOURNAL	J. Biol. Chem. 264 (19), 11387-11393 (1989)	
MEDLINE	89291894	
PUBMED	2738070	
COMMENT	Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Ircin, 23-JUN-1989.	
FEATURES	Location/Qualifiers	
SOURCE	1..951	
	/organism="Bos taurus"	
	/db_xref="taxon:9913"	
	19..462	
	/note="lysozyme 2b precursor"	
	/codon_start=1	
	/protein_id="AAA30629.1"	
	/db_xref="GI:163317"	
	/translation="MKALVILGLFLFSVAVQKVFEECEELARLLKKIGLDGKYGVSLA"	

sig_peptide	19..72	NM1C1KXESSYNRKATYNNRNSSESTDGIQI0NSKMCNDGKTPNADGCHVCSSEI		
mat_peptide	73..459	MENDIKAKVACAKHIVSQGITAWAMKSHCRDHDVSYVBGTL"		
BASE COUNT	294 a	162 c	194 g	301 t
ORIGIN				
Query Match	100.0%;	Score 444;	DB 4;	Length 951;
Best Local Similarity	100.0%;	Pred. No. 6.4e-249;		
Matches 444;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
OY	1	ATGAAGGCTCCGTTATTTCTGGGGTTTCTCTTCCTTTCTGCGCTGCCAAGGAGGTC	60	
Db	19	ATGAAGGCTCCGTTATTTCTGGGGTTTCTTCCTTTCTGCGCTGCCAAGGAGGTC	78	
OY	61	TTTGAGAGATGTGAGCTTGCCAGAACTGTGAAGAACTTGGACTGAGCGCTATPAAGGA	120	
Db	79	TTTGAGAGATGTGAGCTTGCCAGAACTGTGAAGAACTTGGACTGAGCGCTATPAAGGA	138	
OY	121	GTCAGCCCTCGAAACTGGTGTGTTTGACCAATGGGAAAGACAGTTATPAACAAAAAGCT	180	
Db	139	GTCAGCCCTCGAAACTGGTGTGTTTGACCAAAATGGGAAAGACAGTTATPAACAAAAAGCT	198	
OY	181	ACAAACTPACATCTCTAGCAGTGAAGACAGCTGATTTAGGATATTTTCAGATCAACAGCAA	240	
Db	199	ACAAACTPACATCTCTAGCAGTGAAGACAGCTGATTTAGGATATTTTCAGATCAACAGCAA	258	
OY	241	TGTTGGTGTATGATGAGCAAAACCCCTATGTCAGTTGACGGCTGTCATGTATCTCGAGC	300	
Db	259	TGTTGGTGTATGATGAGCAAAACCCCTATGTCAGTTGACGGCTGTCATGTATCTCGAGC	318	
OY	301	GAATTAATGAAAAATGACATCGCTPAAGCTGTAGCGTGTGCAAGACATATTGTCAGTGAG	360	
Db	319	GAATTAATGAAAAATGACATCGCTPAAGCTGTAGCGTGTGCAAGACATATTGTCAGTGAG	378	
OY	361	CAAGGCATTAAGCGCTGGGTGGCAGTNGAAAAAGTCATTGTGAGACCATAGACGTACAGCT	420	
Db	379	CAAGGCATTAAGCGCTGGGTGGCAGTNGAAAAAGTCATTGTGAGACCATAGACGTACAGCT	438	
OY	421	TACGTTGAGGGTTCACCCCTGTAA	444	
Db	439	TACGTTGAGGGTTCACCCCTGTAA	462	
RESULT 3				
BOVLIZYM7A				
LOCUS	BOVLIZYM7A	1060 bp	mRNA	linear
DEFINITION	Bos taurus lysozyme 7A mRNA.			MAM 10-MAR-1994
ACCESSION	U23758			
VERSION	1.23758.1	GI:387905		
KEYWORDS	lysozyme.			
SOURCE	Bos taurus (cow).			
ORGANISM	Bos taurus			
REFERENCE	Eukaryotes: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.			
AUTHORS	1 (bases 1 to 1060)			
TITLE	Takeuchi,K., Irwin,D.M., Gallup,M., Shinbrot,E., Kal,H., Stewart,C.B. and Basbaum,C.			
JOURNAL	Multiple cDNA sequences of bovine tracheal lysozyme			
MEDLINE	J. Biol. Chem. 268 (36), 27440-27446 (1993)			
PUBMED	94086565			
FEATURES	8262986			
SOURCE	Location/Qualifiers			
	1..1060			
	/organism="Bos taurus"			
	/db_xref="taxon:.9913"			
	/cell_type="epithelial/ gland"			
	/tissue_type="trachea"			
	/dev_stage="adult"			
BASE COUNT	337 a	181 c	223 g	319 t

ORIGIN

Query Match 100.0%; Score 444; DB 4; Length 1060;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-249;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTGCTATATTCCTGAGGTTCTCTTCTCTTCTGCTGCTTCCCAAGCAGATC 60  
 DB 118 ATGAAGGCTCTGCTATATTCCTGAGGTTCTCTTCTCTTCTGCTGCTTCCCAAGCAGATC 177

QY 61 TTTGAGAGATGTGAGCTTCCAGACTCTGAGAGAACTTGAGCTGAGCGCTTAAGGA 120  
 DB 178 TTTGAGAGATGTGAGCTTCCAGACTCTGAGAGAACTTGAGCTGAGCGCTTAAGGA 237

QY 121 GTGAGCTGGCAAACTGTTGTGTGACCAATGGAAGCAAGCTATATTAACAAAGAT 180  
 DB 238 GTGAGCTGGCAAACTGTTGTGTGACCAATGGAAGCAAGCTATATTAACAAAGAT 297

QY 181 ACAAACTACAACTCTGAGTGAAGCACTGATTAATGATTTGATCAACACAGAA 240  
 DB 298 ACAAACTACAACTCTGAGTGAAGCACTGATTAATGATTTGATCAACACAGAA 357

QY 241 TGGTGTGATGATGAGCAAAACCCCTAATGAGCTGAGCGCTGATGATCTGACG 300  
 DB 358 TGGTGTGATGATGAGCAAAACCCCTAATGAGCTGAGCGCTGATGATCTGACG 417

QY 301 GAATTAATGAGAAATGACATCGCTAAGCTGAGCGTGCAGCAAGATATGCTAGTGA 360  
 DB 418 GAATTAATGAGAAATGACATCGCTAAGCTGAGCGTGCAGCAAGATATGCTAGTGA 477

QY 361 CAAGCATTTACAGCTGCTGCTGAGCAAGAAAGTCATTGTCGAGCAGTCACTGAC 420  
 DB 478 CAAGCATTTACAGCTGCTGCTGAGCAAGAAAGTCATTGTCGAGCAGTCACTGAC 537

QY 421 TACGTGAGGCTGACACCTGTAA 444  
 DB 538 TACGTGAGGCTGACACCTGTAA 561

RESULT 4  
 LOCUS 112256 964 bp DNA linear PAT 26-JUL-1995  
 DEFINITION Sequence 1 from patent US 5422108.  
 ACCESSION 112256  
 VERSION 112256.1 GI:910279  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 964)  
 AUTHORS Murkov,T.Erik, and Fitzmaurice,L.C.  
 TITLE Protection of plants against plant pathogens  
 JOURNAL Patent: US 5422108-A 1 06-JUN-1995;  
 FEATURES  
 source Location/Qualifiers  
 1. 964  
 /organism="Unknown"  
 BASE COUNT 297 a 165 c 201 g 301 t  
 ORIGIN

Query Match 98.9%; Score 439; DB 6; Length 964;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-246;  
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCCTGCTATATTCCTGAGGTTCTCTTCTCTTCTGCTGCTGCTCAAGCAGATCTTGA 65  
 DB 24 GGCCTGCTATATTCCTGAGGTTCTCTTCTCTTCTGCTGCTGCTCAAGCAGATCTTGA 83

QY 66 GAGATGTGAGCTGAGCACTGAGAACTTGAGCTGAGCGCTATTAAGGAGTCAAG 125  
 DB 84 GAGATGTGAGCTGAGCACTGAGAACTTGAGCTGAGCGCTATTAAGGAGTCAAG 143

QY 126 CTTGGCAAACTGCTGTGTTGACCAATGGAAGCAAGTATTAACAAAGCTACAA 185  
 DB 126 CTTGGCAAACTGCTGTGTTGACCAATGGAAGCAAGTATTAACAAAGCTACAA 185

DB 144 CTTGGCAAACTGCTGTGTTGACCAATGGAAGCAAGTATTAACAAAGCTACAA 203

QY 186 CTACAACTCTGAGCTGAGAAAGCACTGATTAATGCAATTTGAGTCAACAGCAATG 245  
 DB 204 CTACAACTCTGAGCTGAGAAAGCACTGATTAATGCAATTTGAGTCAACAGCAATG 263

QY 246 GTGTATGATGTGCAAAACCCCTAATGAGCTGAGCGCTGATGATCTGACAGAAAT 305  
 DB 264 GTGTATGATGTGCAAAACCCCTAATGAGCTGAGCGCTGATGATCTGACAGAAAT 323

QY 306 AATGAAAATGACATGCTAAAGCTGATGAGCTGTCGCAAGCAATTTGCTAGTGA 365  
 DB 324 AATGAAAATGACATGCTAAAGCTGATGAGCTGTCGCAAGCAATTTGCTAGTGA 383

QY 366 CATTCAGCGCTGAGGCAATGGAAGCAATTTGCAAGCAATGAGTCAAGTACAGT 425  
 DB 384 CATTCAGCGCTGAGGCAATGGAAGCAATTTGCAAGCAATGAGTCAAGTACAGT 443

QY 426 TGAGGTTGCAACCTGTAA 444  
 DB 444 TGAGGTTGCAACCTGTAA 462

RESULT 5  
 LOCUS BOVLSZ2A 909 bp mRNA linear MAM 27-APR-1993  
 DEFINITION Bovine lysozyme C isozyme 2a mRNA, complete cds.  
 ACCESSION M6241 J04831 M27181  
 VERSION M6241.1 GI:163314  
 KEYWORDS  
 SOURCE Bovine abomasum, cDNA to mRNA, clone lambda-cb1.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 909)  
 AUTHORS Irwin,D.M. and Wilson,A.C.  
 TITLE Multiple cDNA sequences and the evolution of bovine stomach  
 lysozyme  
 JOURNAL J. Biol. Chem. 264 (19), 11387-11393 (1989)  
 MEDLINE 89281894  
 PUBMED 2738070  
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
 by D.M. Irwin, 23-JUN-1989.  
 FEATURES  
 source Location/Qualifiers  
 1. 909  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
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 /note="Lysozyme 2a precursor"  
 /codon\_start=2  
 /protein\_id="AAA30628.1"  
 /db\_xref="GI:163315"  
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 LCIITWESYNTKATNPNSSSESTDYGFQIINSKWCMDGKTPNVDGCHVSCSEIME  
 NDIKAVACAKHIVSEGGITLAVMKSHCRDHDVSYEGCTL"  
 <1. 49  
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 50. 436  
 /product="Lysozyme 2a"  
 154 c 187 g 286 t  
 BASE COUNT 282 a 154 c 187 g 286 t  
 ORIGIN

Query Match 98.4%; Score 437; DB 4; Length 909;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-245;  
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTTCTGCTATATTCCTGAGGTTCTCTTCTCTTCTGCTGCTGCTCAAGCAGATCTTGA 67  
 DB 3 CTTCTGCTATATTCCTGAGGTTCTCTTCTCTTCTGCTGCTGCTCAAGCAGATCTTGA 62

QY 68 GATGTGAGCTGAGCACTGAGAACTTGAGCTGAGCGCTATTAAGGAGTCAAGC 127  
 DB 68 GATGTGAGCTGAGCACTGAGAACTTGAGCTGAGCGCTATTAAGGAGTCAAGC 127

Db	63	GATGAGACCTTGCCAGACACTCTGGAAGAAACTTGGACCTGACGGCGTATTAAGGAGTCAACC	122
QY	128	TGGCAAACTGGTGTGTGTTGACCAATGGGAAAGCAGTTATPACAAAGCTACAACT	187
Db	123	TGGCAAACTGGTGTGTGTTGACCAATGGGAAAGCAGTTATPACAAAGCTACAACT	182
QY	188	ACAATCCAGACAGTGAAGACACTGTATATGGGATTTTCAGATCAACAGCAAAATGGTGGT	247
Db	183	ACAATCCAGACAGTGAAGACACTGTATATGGGATTTTCAGATCAACAGCAAAATGGTGGT	242
QY	248	GTAATGATGSCAAAACCCCTAATGACAGTTGACGGCTGTCAATGATCTGCAGCGAATTAA	307
Db	243	GTAATGATGSCAAAACCCCTAATGACAGTTGACGGCTGTCAATGATCTGCAGCGAATTAA	302
QY	308	TGGAAAATGACATGGCTTAAGCTGAGCGGTGTCGAAAGCATATTTGCTAGTGAAGCA	367
Db	303	TGGAAAATGACATGGCTTAAGCTGAGCGGTGTCGAAAGCATATTTGCTAGTGAAGCA	362
QY	368	TTACAGCCTGGGTGGCATGATGAAAAGTCATTGTGACAGCCATGACGTACAGATTACGTTG	427
Db	363	TTACAGCCTGGGTGGCATGATGAAAAGTCATTGTGACAGCCATGACGTACAGATTACGTTG	422
QY	428	AGGCTTGACACCTGTAA 444	
Db	423	AGGCTTGACACCTGTAA 439	
RESULT 6			
LOCUS	109315	109315	963 bp
DEFINITION	Sequence 1 from Patent WO 8904320.		
ACCESSION	109315		
VERSION	109315.1	GI:587976	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 963)		
TITLE	Digan,M.E., Harpold,M.W., Iatr,S.V., Thill,G.P., Siegel,R.S., Ellis,S.B. and Williams,M.E.		
JOURNAL	PRODUCTION OF ANIMAL LYSOZYME c VIA SECRETION FROM PICHIA PASTORIS		
FEATURES	AND COMPOSITION THEREFOR		
source	Patent: WO 8904320-A 1 18-MAY-1989;		
	Location/Qualifiers		
	1..963		
BASE COUNT	/organism="unknown"		
ORIGIN	298 a	165 c	200 g 299 t 1 others
Query Match	98.4%; Score 437; DB 6; Length 963;		
Best Local Similarity	100.0%; Pred. No. 8.2e-245;		
Matches 437;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	8	CTCTCGTATTCTGGGGTTTCTCTTCCTTTCTGTGCTGTCCAAAGCAGGCTTTTGAGA	67
Db	26	CTCTCGTATTCTGGGGTTTCTCTTCCTTTCTGTGCTGTCCAAAGCAGGCTTTTGAGA	85
QY	68	GATGTGAGCTTGCAGAACTGTGAAGAACTTGGACGTGAGAGGCTATPAAAGGATCGCC	127
Db	86	GATGTGAGCTTGCAGAACTGTGAAGAACTTGGACGTGAGAGGCTATPAAAGGATCGCC	145
QY	128	TGGCAAACTGGTGTGTTGACCAAAATGGGAAAGCAGTTATPACAAAGCTACAACT	187
Db	146	TGGCAAACTGGTGTGTTGACCAAAATGGGAAAGCAGTTATPACAAAGCTACAACT	205
QY	188	ACAATCTAGCAGTGAAGACACTGATATATGGGATTTTCAGATCAACAGCAAAATGGTGGT	247
Db	206	ACAATCTAGCAGTGAAGACACTGATATATGGGATTTTCAGATCAACAGCAAAATGGTGGT	265
QY	248	GTAATGATGSCAAAACCCCTAATGACAGTTGACGGCTGTCAATGATCTGCAGCGAATTAA	307
Db	266	GTAATGATGSCAAAACCCCTAATGACAGTTGACGGCTGTCAATGATCTGCAGCGAATTAA	325

QY	308	TGGAANAATGCATGCTAAACCTGTAGCGTGTGCAAAGCATATGTCTAGTACGAAGCA	367
Db	326	TGGAANAATGCATGCTAAACCTGTAGCGTGTGCAAAGCATATGTCTAGTACGAAGCA	385
QY	368	TTACAGCCTGGGTGGCATGAGAAAGTCATTTCTCAGACATGACGTACAGTACGTTG	427
Db	386	TTACAGCCTGGGTGGCATGAGAAAGTCATTTCTCAGACATGACGTACAGTACGTTG	445
QY	428	AGGTTGCACCCCTGTAA 444	
Db	446	AGGTTGCACCCCTGTAA 462	
RESULT 7			
LOCUS	BOVLSZ2C	877 bp	mRNA linear MAM 27-APR-1993
DEFINITION	Bovine lysozyme c isozyme 2c mRNA, complete cds.		
ACCESSION	M26244 J04831 M27183		
VERSION	M26244.1 GI:163318		
KEYWORDS	lysozyme.		
SOURCE	Bovine albumosum, cDNA to mRNA, clones lambda-cBL[20,36,39].		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;		
	Bovidae; Bovinae; Bos.		
	1 (bases 1 to 877)		
REFERENCE	Irwin,D.M. and Wilson,A.C.		
AUTHORS	Multiple cDNA sequences and the evolution of bovine stomach		
TITLE	lysozyme		
JOURNAL	J. Biol. Chem. 264 (19), 11387-11393 (1989)		
MEDLINE	89291894		
PUBMED	2738070		
COMMENT	Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 23-JUN-1989.		
FEATURES	Location/Qualifiers		
source	1..877		
	/organism="Bos taurus"		
	/db_xref="taxon:9913"		
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CDS	/note="lysozyme 2c precursor"		
	/codon_start=1		
	/protein_id="AAA30630.1"		
	/db_xref="GI:163319"		
	/translation="VKGVKPERELATLTKRLGIDGKGVSIANMLCTFKWESSYNRK		
	ATNWNPSSESDYGIROIINSKRCMNCKCTPNAYNDGCHVSCSELMENDIAAIVACAKHII		
	VSESGITAWYAAWSKCHDHDVSVIVECITL"		
	<1..9		
	/note="lysozyme 2c signal peptide"		
	10..396		
	/product="lysozyme 2c"		
BASE COUNT	285 a 142 c 181 g 269 t		
ORIGIN			
Query Match	89.0%; Score 395; DB 4; Length 877;		
Best Local Similarity	100.0%; Pred. No. 3.8e-220;		
Matches	395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	50	AAGGCAAGGCTTTGAGAGATGTGACGCTTGCCAGCAACTCTGGAAGAAACTGGACTGCAGC	109
Db	5	AAGGCAAGGCTTTGAGAGATGTGACGCTTGCCAGCAACTCTGGAAGAAACTGGACTGCAGC	64
QY	110	GCTATTAAGGAGAGTCAGCTGGCAAAACGTTGTGTTGTGACCAATGGGAAGCAGTTATA	169
Db	65	GCTATTAAGGAGAGTCAGCTGGCAAAACGTTGTGTTGTGACCAATGGGAAGCAGTTATA	124
QY	170	ACACAAAAGCTACAACTACATCTCAGACAGTGAAGAACTGATTTATGGATATTTCAGA	229
Db	125	ACACAAAAGCTACAACTACATCTCAGACAGTGAAGAACTGATTTATGGATATTTCAGA	184
QY	230	TCAACAGCAATGTGTGTTAAATGATGTGGCAAAACCCCTATATGACAGTTGAGCGCTGTATG	289
Db	185	TCAACAGCAATGTGTGTTAAATGATGTGGCAAAACCCCTATATGACAGTTGAGCGCTGTATG	244

QY 290 TATCTGCAGCGAATTAATGAAATGACATGCTAAGCTGTAGCTGTGCAAGACATA 349  
| | | | |  
DB 245 TATCTGCAGCGAATTAATGAAATGACATGCTAAGCTGTAGCTGTGCAAGACATA 304  
| | | | |  
QY 350 TTGTCACTAGTACGCAAGCATTACAGCTGGGTGATGCAAAAGTCTTGTGCAAGACATG 409  
| | | | |  
DB 305 TTGTCACTAGTACGCAAGCATTACAGCTGGGTGATGCAAAAGTCTTGTGCAAGACATG 364  
| | | | |  
QY 410 ACCTCAGCAGTTAGCTGTGAGGGTTCGACCCCTGTAA 444  
| | | | |  
DB 365 ACCTCAGCAGTTAGCTGTGAGGGTTCGACCCCTGTAA 399  
| | | | |

## RESULT 8

LOCUS BOVIS222A 786 bp mRNA linear MAM 27-APR-1993  
DEFINITION Bovine lysozyme c isozyme 2d mRNA, complete cds.  
ACCESSION M26240.1 J04831 M27184  
VERSION M26240.1 GI:163320  
KEYWORDS lysozyme.  
SOURCE Bovine abomasum, cDNA to mRNA, clone lambda-cBL29.  
ORGANISM Bos taurus

## REFERENCE

AUTHORS Irwin,D.M. and Wilson,A.C.  
TITLE Multiple cDNA sequences and the evolution of bovine stomach  
JOURNAL lysozyme  
MEDLINE J. Biol. Chem. 264 (19), 11387-11393 (1989)  
PUBMED 89291894  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M. Irwin, 23-JUN-1989.

## FEATURES

source  
location/Qualifiers  
1..786  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
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/translation="ASWILCTKMESSYNTKATYNPSSSESTDIYGIQINSKWCNDGK  
TPNAVDCCHSCSEIMENDIAKAVAKAKHIVSEQGITAWAMKSHCRDHDVSSYVSGC  
TL"

## BASE COUNT

256 a 127 c 154 g 249 t

## ORIGIN

Query Match 69.8%; Score 310; DB 4; Length 786;  
Best Local Similarity 100.0%; Pred. No. 3e-170;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 CTGGTGTGTTTGGACCAATGGAAGACAGTTATACACAAAGCTACAACTACATCC 194  
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DB 7 CTGGTGTGTTTGGACCAATGGAAGACAGTTATACACAAAGCTACAACTACATCC 66  
| | | | |  
QY 195 TAGCAGTGAAGCAGCTATTTGGGATTTTTCAGATCAACAGCAATGGTGTATGA 254  
| | | | |  
DB 67 TAGCAGTGAAGCAGCTATTTGGGATTTTTCAGATCAACAGCAATGGTGTATGA 126  
| | | | |  
QY 255 TGGCAAAACCCCTAATGAGTGTGACGGCTGTATGATTCCTGACGCAATTAATGAAA 314  
| | | | |  
DB 127 TGGCAAAACCCCTAATGAGTGTGACGGCTGTATGATTCCTGACGCAATTAATGAAA 186  
| | | | |  
QY 315 TGACATGCTAAAGCTGTAGCGTGTGCAAAAGCATATTTGAGTAGAGGATTAACG 374  
| | | | |  
DB 187 TGACATGCTAAAGCTGTAGCGTGTGCAAAAGCATATTTGAGTAGAGGATTAACG 246  
| | | | |  
QY 375 CTGGGTGATGAGAAAGTCAATTTGAGAGCAGTACAGCTTACGTTAGGGGTG 434  
| | | | |  
DB 247 CTGGGTGATGAGAAAGTCAATTTGAGAGCAGTACAGCTTACGTTAGGGGTG 306  
| | | | |

QY 435 CACCTGTAA 444  
| | | | |  
DB 307 CACCTGTAA 316  
| | | | |

## RESULT 9

LOCUS BOVIS23A 1082 bp mRNA linear MAM 27-APR-1993  
DEFINITION Bovine lysozyme c isozyme 3a mRNA, complete cds.  
ACCESSION M26242.1 J04831 M27180  
VERSION M26242.1 GI:163322  
KEYWORDS lysozyme.  
SOURCE Bovine abomasum, cDNA to mRNA, clone lambda-cBL[26,28].  
ORGANISM Bos taurus

## REFERENCE

AUTHORS Irwin,D.M. and Wilson,A.C.  
TITLE Multiple cDNA sequences and the evolution of bovine stomach  
JOURNAL lysozyme  
MEDLINE J. Biol. Chem. 264 (19), 11387-11393 (1989)  
PUBMED 89291894  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M. Irwin, 23-JUN-1989.

## FEATURES

source  
location/Qualifiers  
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/organism="Bos taurus"  
/db\_xref="taxon:9913"  
9..452  
/note="lysozyme 3a precursor"  
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/db\_xref="GI:163323"  
/translation="MKALLIGFLSLVAVGKPEREELARTLKLGLDGYKSYLA  
NMWILCTKMESSYNTKATYNPSSSESTDIYGIQINSKWCNDGKTPNAVDCCHSCSEL  
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## BASE COUNT

343 a 205 c 209 g 325 t

## ORIGIN

Query Match 45.5%; Score 202; DB 4; Length 1082;  
Best Local Similarity 99.6%; Pred. No. 7.8e-107;  
Matches 252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TTATCTGGGGTTCCTTCCTTCCTGCTGCTCCAAAGCAAGCTTTGAGAGATGTG 73  
| | | | |  
DB 22 TTATCTGGGGTTCCTTCCTTCCTGCTGCTCCAAAGCAAGCTTTGAGAGATGTG 81  
| | | | |  
QY 74 AGCTGCCAGAACTGTGAAGAACTTGAAGTGAAGGCTATTAAGGAGTACCGTGCNA 133  
| | | | |  
DB 82 AGCTGCCAGAACTGTGAAGAACTTGAAGTGAAGGCTATTAAGGAGTACCGTGCNA 141  
| | | | |  
QY 134 ACTGCTGTGTTTGGACCAATGGAAGAGTATTAACCAAAAGCTACAACTCAATC 193  
| | | | |  
DB 142 ACTGCTGTGTTTGGACCAATGGAAGAGTATTAACCAAAAGCTACAACTCAATC 201  
| | | | |  
QY 194 CTAGCAGTGAAGCACTGATTTATGGGATTTTTCAGATCAACAGCAATGGTGTATG 253  
| | | | |  
DB 202 CTAGCAGTGAAGCACTGATTTATGGGATTTTTCAGATCAACAGCAATGGTGTATG 261  
| | | | |  
QY 254 ATGGCAAAACCC 266  
| | | | |  
DB 262 ATGGCAAAACCC 274  
| | | | |

## RESULT 10

LOCUS BOVIS20ZMB 10212 bp DNA linear MAM 29-OCT-1993

DEFINITION Bos taurus lysozyme gene (cow 2), complete cds.  
 ACCESSION M95098  
 VERSION M95098.1 GI:163331  
 KEYWORDS lysozyme; repetitive DNA.  
 SOURCE Bos taurus DNA.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 10212)  
 Irwin,D.M., White,R.T. and Wilson,A.C.  
 Characterization of the cow stomach lysozyme genes: repetitive DNA and concerted evolution  
 JOURNAL J. Mol. Evol. 37 (4), 355-366 (1993)  
 MEDLINE 94141937  
 PUBMED 8308905  
 FEATURES  
 source location/Qualifiers  
 1..10212  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 218..511  
 /note="putative"  
 /rpt\_family="Nla"  
 /rpt\_type="dispersed"  
 2506..8130  
 /gene="lysozyme"  
 join(2506..2672,3840..4004,6136..6211,7575..8130)  
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 2506..2672  
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 /number=1  
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 join(2537..2672,3840..4004,6136..6211,7575..7641)  
 /gene="lysozyme"  
 /codon\_start=1  
 /product="lysozyme"  
 /protein\_id="AAC37311.1"  
 /db\_xref="GI:163332"  
 /translation="MKALVILGFLFLSVAVGKVERCELARTLKLGIDGKGVSLA  
 NMCLTQWESSYNTKATNPNPSSSESDYGIPOINSKMCNDGKTNPNAVDCGHSVSEL  
 MENDIAKAVACAKHIYSEOGITAMVAMKSHCRHDVSSIVGECTL"  
 3840..4004  
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 /note="putative"  
 /number=2  
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 4113..4238  
 /gene="lysozyme"  
 /note="putative"  
 /rpt\_family="Bovine Consensus Sequence (BCS)"  
 /rpt\_type="dispersed"  
 4381..4510  
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 /note="putative"  
 /number=3  
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 7575..8130  
 /gene="lysozyme"  
 /note="putative"  
 /number=4  
 /label-exon4  
 3031 a 1982 c 1909 g 3290 t

ORIGIN  
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 Best Local Similarity 100.0%; Pred. NO. 4e-85;  
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 137 GGTGCGTTTGACCAATGGGAAAGACAGTTATACACAAAGCTACAACTACAACTCCTA 196  
 |||||||  
 Db 3840 GGTGTGTTTGACCAATGGGAAAGACAGTTATACACAAAGCTACAACTACAACTCCTA 3899  
 |||||||  
 QY 197 GCAGTGAAGACACGTATATGGGATATTTTCAGATCAACAGCAAAATGTTGTAATGATG 256  
 |||||||  
 Db 3900 GCAGTGAAGACACGTATATGGGATATTTTCAGATCAACAGCAAAATGTTGTAATGATG 3959  
 |||||||  
 QY 257 GCAGTGAAGACACGTATATGGGATATTTTCAGATCAACAGCAAAATGTTGTAATGATG 301  
 |||||||  
 Db 3960 GCAGTGAAGACACGTATATGGGATATTTTCAGATCAACAGCAAAATGTTGTAATGATG 4004  
 |||||||  
 RESULT 11  
 BOVLYSOZMC 8051 bp DNA linear MAM 29-OCT-1993  
 LOCUS BOVLYSOZMC  
 DEFINITION Bos taurus lysozyme gene (cow 3), complete cds.  
 ACCESSION M95099  
 VERSION M95099.1 GI:163333  
 KEYWORDS lysozyme; repetitive DNA.  
 SOURCE Bos taurus DNA.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 8051)  
 Irwin,D.M., White,R.T. and Wilson,A.C.  
 Characterization of the cow stomach lysozyme genes: repetitive DNA and concerted evolution  
 JOURNAL J. Mol. Evol. 37 (4), 355-366 (1993)  
 MEDLINE 94141937  
 PUBMED 8308905  
 FEATURES  
 source location/Qualifiers  
 1..8051  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
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 716..904  
 /note="putative"  
 /number=1  
 /label-exon1  
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 MENDIAKAVACAKHIYSEOGITAMVAMKSHCRHDVSSIVGECTL"  
 2158..2322  
 /gene="lysozyme"  
 /product="lysozyme"  
 /note="putative"  
 /label-exon2  
 3645..3771  
 /gene="lysozyme"  
 /note="putative"  
 /rpt\_family="Bovine Consensus Sequence (BCS)"  
 /rpt\_type="dispersed"  
 4118..4193  
 /gene="lysozyme"  
 /product="lysozyme"

/note="putative"  
/label=exon3  
4352..4625  
/gene="lysozyme"  
/note="putative"  
/rpl\_family="BCS dimer"  
/rpl\_type="dispersed"  
5308..6746  
/gene="lysozyme"  
/note="putative"  
/rpl\_family="Art2 plus approx 900 bp unique"  
/rpl\_type="dispersed"  
7192..7755  
/gene="lysozyme"  
/note="putative"  
/number=4  
/label=exon4

BASE COUNT 2412 a 1453 c 1457 g 2729 t

ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 130; DB 4; Length 8051;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 GGTGTGTTGACCAATGGGAAGCAGTTATTAACAAAGCTACCAATCAATCTTA 196  
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Db 2158 GGTGTGTTGACCAATGGGAAGCAGTTATTAACAAAGCTACCAATCAATCTTA 2217  
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QY 197 GCAGTGAAGCACTGATTTATGGATTTTCAGATCAACGCAAAATGGTGTATGATG 256  
|||||  
Db 2218 GCAGTGAAGCACTGATTTATGGATTTTCAGATCAACGCAAAATGGTGTATGATG 2277  
|||||

QY 257 GCAAAACCCC 266  
|||||  
Db 2278 GCAAAACCCC 2287  
|||||

RESULT 12  
SHP12M1B 881 bp mRNA linear MAM 27-APR-1993  
LOCUS  
DEFINITION Sheep lysozyme 1b (Lzmb1b) mRNA, 3' end.  
ACCESSION M32493.1 J05279  
VERSION M32493.1 GI:165965  
KEYWORDS  
SOURCE Sheep abomasum, cDNA to mRNA.  
ORGANISM  
Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
1 (bases 1 to 881)  
Irwin,D.M. and Wilson,A.C.  
Concerted evolution of ruminant stomach lysozymes. Characterization  
of lysozyme cDNA clones from sheep and deer  
J. Biol. Chem. 265 (9), 4944-4952 (1990)

JOURNAL  
MEDLINE  
PUBMED  
2318875  
90202968

COMMENT  
Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M.Irwin, 01-MAR-1990.

FEATURES  
Location/Qualifiers  
source  
1..881  
/organism="Ovis aries"  
/db\_xref="taxon:9940"  
<1..390  
/note="lysozyme 1b precursor"  
/codon\_start=1  
/protein\_id="AAA31558.1"  
/db\_xref="GI:165965"  
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YNPGESEIDYGIFOJNSKMWKNDGKTPNAVVDGCHVSCSELMENNIARAKAVCAKHIVSE  
OGITAWVAWKRSHCRDHDVSSVVEGCSL"  
1..387  
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1..387  
/product="lysozyme 1b"  
1..17  
misc\_feature

CDS  
1..390  
/note="lysozyme 1b precursor"  
/codon\_start=1  
/protein\_id="AAA31558.1"  
/db\_xref="GI:165965"  
/translation="KFERCELARTLKEIGLDGKGVSLANMLCLTKWESSYNTKATN  
YNPGESEIDYGIFOJNSKMWKNDGKTPNAVVDGCHVSCSELMENNIARAKAVCAKHIVSE  
OGITAWVAWKRSHCRDHDVSSVVEGCSL"  
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1..387  
/product="lysozyme 1b"  
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misc\_feature

/note="PCR primer"  
BASE COUNT 285 a 145 c 182 g 269 t

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Query Match  
Best Local Similarity 100.0%; Score 96; DB 4; Length 881;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 GCACGTGACGGCTATTAAGGAGTACGCTGGCAAACTGGTTGTTTACCAATGGGAA 159  
|||||  
Db 46 GCACGTGACGGCTATTAAGGAGTACGCTGGCAAACTGGTTGTTTACCAATGGGAA 105  
|||||

QY 160 AGCAGTTATTAACAAAGCTACCAATCAATCTCT 195  
|||||  
Db 106 AGCAGTTATTAACAAAGCTACCAATCAATCTCT 141  
|||||

RESULT 13  
SHP12M1C 881 bp mRNA linear MAM 27-APR-1993  
LOCUS  
DEFINITION Sheep lysozyme 1c (lyz1c) mRNA, 3' end.  
ACCESSION M32494.1 J05279  
VERSION M32494.1 GI:165967  
KEYWORDS  
SOURCE Sheep abomasum, cDNA to mRNA.  
ORGANISM  
Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
1 (bases 1 to 881)  
Irwin,D.M. and Wilson,A.C.  
Concerted evolution of ruminant stomach lysozymes. Characterization  
of lysozyme cDNA clones from sheep and deer  
J. Biol. Chem. 265 (9), 4944-4952 (1990)

JOURNAL  
MEDLINE  
PUBMED  
2318875  
90202968

COMMENT  
Draft entry and computer-readable sequence for [1] kindly submitted  
by D.M.Irwin, 01-MAR-1990.

FEATURES  
Location/Qualifiers  
source  
1..881  
/organism="Ovis aries"  
/db\_xref="taxon:9940"  
<1..390  
/note="lysozyme 1c precursor"  
/codon\_start=1  
/protein\_id="AAA31559.1"  
/db\_xref="GI:165968"  
/translation="KFERCELARTLKEIGLDGKGVSLANMLCLTKWESSYNTKATN  
YNPGESEIDYGIFOJNSKMWKNDGKTPNAVVDGCHVSCSELMENNIARAKAVCAKHIVSE  
OGITAWVAWKRSHCRDHDVSSVVEGCSL"  
1..387  
mat\_peptide  
1..17  
misc\_feature  
1..17  
/note="PCR primer"  
BASE COUNT 285 a 144 c 183 g 269 t

ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 96; DB 4; Length 881;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 GCACGTGACGGCTATTAAGGAGTACGCTGGCAAACTGGTTGTTTACCAATGGGAA 159  
|||||  
Db 46 GCACGTGACGGCTATTAAGGAGTACGCTGGCAAACTGGTTGTTTACCAATGGGAA 105  
|||||

QY 160 AGCAGTTATTAACAAAGCTACCAATCAATCTCT 195  
|||||  
Db 106 AGCAGTTATTAACAAAGCTACCAATCAATCTCT 141  
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RESULT 14  
SHP12M2A 881 bp mRNA linear MAM 27-APR-1993  
LOCUS





Query Match	Best Local Similarity	100.0%	Score 444;	DB 24;	Length 444;
Matches 444;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAGCTCTCGTATTATCTGGGGTTTCTCTCTCTTCTGTCGTGTCACGAAGGCAAGGTC	60		
Db	1	ATGAAGGCTCTCGTATTATCTGGGGTTTCTCTCTCTTCTGTCGTGTCACGAAGGCAAGGTC	60		
QY	61	TTTGAGAGATGTGACCTTGCCAGAACTCTGAAGAACTTGAGACTGAGGGCTATTAAGGGA	120		
Db	61	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGAGACTGAGGGCTATTAAGGGA	120		
QY	121	GTCAGCTTGGCAAACTGGTGTGTGTTGAACCAATGGGAAGACAGTTATPACACAAAAGCT	180		
Db	121	GTCAGCTTGGCAAACTGGTGTGTGTTGAACCAATGGGAAGACAGTTATPACACAAAAGCT	180		
QY	181	ACAAACTCATATCCAGACGTGAAGACACTGATTTATGGGATATTTCAGATCAACGACAAA	240		
Db	181	ACAAACTCATATCCAGACGTGAAGACACTGATTTATGGGATATTTCAGATCAACGACAAA	240		
QY	241	TGTTGGTGTATATGATGGCAAAACCCCTTAATSCAGTTGACGGCTGTATATTCCTGCAGC	300		
Db	241	TGTTGGTGTATATGATGGCAAAACCCCTTAATSCAGTTGACGGCTGTATATTCCTGCAGC	300		
QY	301	GAATTAAATGAGAAATGATAGCTTAAGCTGTAGCGTGTGCAAAAGCATATTGTCACTAG	360		
Db	301	GAATTAAATGAGAAATGATAGCTTAAGCTGTAGCGTGTGCAAAAGCATATTGTCACTAG	360		
QY	361	CAAGGCAATTAAGCGCTGGGTGGCATATGCAAAAGTCAATTCGACAGCATAGACGTACAGCT	420		
Db	361	CAAGGCAATTAAGCGCTGGGTGGCATATGCAAAAGTCAATTCGACAGCATAGACGTACAGCT	420		
QY	421	TACGTTGAGGGTGCACCCCTGTAA 444			
Db	421	TACGTTGAGGGTGCACCCCTGTAA 444			

RESULT 2

AAQ05054

ID AAQ05054 standard; DNA; 459 BP.

XX AAQ05054;

AC 30-OCT-1990 (first entry)

DT

XX Sequence encoding bovine Lysozyme c2.

DE

QY	241	TTGGGGGTATATATATGCAAAACCCCTAATGCATGTAGCGGCTGTCAATGTCCTGGAGC	300
Db	6007	TTGGTGTGTATATGATGCGAAACCCCTTAATGCAATTGACGGCTTCATGTCCTGCAGC	6066
QY	301	GAATTATATGCAAAATGACATCGCTTAAGCTGTAGCGTGTGCAGACATATTGTCAGTGAC	360
Db	6067	GAATTATATGCAAAATGACATCGCTTAAGCTGTAGCGTGTGCAGACATATTGTCAGTGAC	6126
QY	361	CAAGGCATTACAGCCTTGGGTGGCATGTGAAAAAGTCATTGTGAGACCATAGACGTAGACGT	420
Db	6127	CAAGGCATTACAGCCTTGGGTGGCATGTGAAAAAGTCATTGTGAGACCATAGACGTAGACGT	6186
QY	421	TACGTTGAGGGTTGCACCCCTGTAA	444
Db	6187	TACGTTGAGGGTTGCACCCCTGTAA	6210
RESULT 4			
AAV08922	AAV08922 standard; cDNA; 964 BP.		
XX	AAV08922;		
AC	26-FEB-1999	(first entry)	
DT	Bovine Lysozyme c2 protein coding sequence.		
XX	Lysozyme; signal peptide; transgenic plant; plant pathogen;		
KW	pathogen resistance; ds.		
XX	Bos sp.		
OS			
XX	Key	Location/Qualifiers	
EH	CDS	25..462	
FT	/*tag= a		
XX	US5850025-A.		
PN	15-DEC-1998.		
PD	22-APR-1997;	97US-0919093.	
XX	12-JAN-1995;	95US-0373390.	
PR	19-SEP-1991;	91US-0762679.	
PR	25-NOV-1991;	91US-0798223.	
PR	22-APR-1997;	97US-0919093.	
XX	(SIBI-) STBIA NEUROSCIENCES INC.		
PA	Fitzmaurice LC, Mirkov TE;		
XX	WPI: 1999-069855/06.		
XX	P-PSDB; AAW73502.		
DR	Transgenic plants resistant to bacterial pathogens - contain		
PT	ruminant Lysozyme gene		
XX	Example 1; Column 37-40; 23pp; English.		
XX	This sequence encodes the bovine lysozyme c2 and can be		
CC	used in the transgenic plant of the invention. The transgenic plant is		
CC	resistant to plant pathogens and contains heterologous DNA encoding a		
CC	ruminant or ruminant-like lysozyme, the plant expresses sufficient levels		
CC	of the lysozyme to render it less susceptible to the pathogens than the		
CC	wild-type plant. The plants are resistant to bacterial pathogens such as		
CC	Pseudomonas syringae or Erwinia carotovora.		
XX	Sequence 964 BP; 297 A; 165 C; 201 G; 301 T; 0 other;		
XX	Query Match 98.9%; Score 439; DB 20; Length 964;		
XX	Best Local Similarity 100.0%; Pred. No. 4.9e-220;		
XX	Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

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QY 6 GGCCTGCTATTTCCTGGGGTTTCCTTCCTTCTGTCGTCGCAAGGCAAGGCTTTGA 65
DB 24 GGCTCTGCTATTTCCTGGGGTTTCCTTCCTTCTGTCGTCGCAAGGCAAGGCTTTGA 83
QY 66 GAGATGTGAGCTTGGCCGAAGACTGTGAAGAACTTGGAGCTGAGCGCTATTAAGGAGTCAG 125
DB 84 GAGATGTGAGCTTGGCCGAAGACTGTGAAGAACTTGGAGCTGAGCGCTATTAAGGAGTCAG 143
QY 126 CCTGGCAAACTGTTGTTGTTGACCAATGGGAAGCAAGTTATTAACCAAAAGCTTCAAA 185
DB 144 CCTGGCAAACTGTTGTTGTTGACCAATGGGAAGCAAGTTATTAACCAAAAGCTTCAAA 203
QY 186 CTACATCTTACGAGTGAAGCACTGATTATGGAATTTTCAGATCAACAGCAATGGTG 245
DB 204 CTACATCTTACGAGTGAAGCACTGATTATGGAATTTTCAGATCAACAGCAATGGTG 263
QY 246 GTGTAATGATGGCAAAACCCCTAATGAGTGAAGGCTGTCATGTAATCCGCGCAAGTT 305
DB 264 GTGTAATGATGGCAAAACCCCTAATGAGTGAAGGCTGTCATGTAATCCGCGCAAGTT 323
QY 306 AATGGAATAATGACATCGCTTAAGCTGAGCGTGTGCAAAAGCATATTGTGAGAGCAAG 365
DB 324 AATGGAATAATGACATCGCTTAAGCTGAGCGTGTGCAAAAGCATATTGTGAGAGCAAG 383
QY 366 CATTACAGCTGGGTGATGCAAAAGTCTTTGTGAGACCATGACGTGACAGTTACGT 425
DB 384 CATTACAGCTGGGTGATGCAAAAGTCTTTGTGAGACCATGACGTGACAGTTACGT 443
QY 426 TGAGGGTTGCACCCCTGTA 444
DB 444 TGAGGGTTGCACCCCTGTA 462

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RESULT 5  
 AAN92057  
 ID AAN92057 standard; DNA; 964 BP.

AC AAN92057;  
 DT 07-APR-1990 (first entry)

DE ss sequence of cDNA insert of clone lambda B13 encoding bovine  
 DE lysozyme C2 together with 3' untranslated region.

KM Bovine lysozyme C2; protein signal sequence; Pinchia pastoris;  
 KM heterologous protein secretion

OS Bovine.

XX

FT Key Location/Qualifiers  
 FT misc-feature 1..23  
 FT misc-feature /tag- a  
 FT misc-feature /standard\_name= "EcoRI Adaptor"  
 FT misc-feature 942..964  
 FT misc-feature /tag- b  
 FT misc-feature /standard\_name= "EcoRI Adaptor"  
 FT misc-feature 25..462  
 FT misc-feature /tag- c  
 FT misc-feature 68..462  
 FT misc-feature /tag- d  
 FT misc-feature 463..964  
 FT misc-feature /tag- e

XX W08904320-A.  
 XX 18-MAY-1989.  
 XX 02-NOV-1988; 88MO-U503907.  
 XX 02-NOV-1987; 87US-0115940.  
 XX (SALK ) SALK INST FOR BIOL STUD.

```

XX 186 CTACATCTTACGAGTGAAGCACTGATTATGGAATTTTCAGATCAACAGCAATGGTG 245
PI Williams ME; Harpold MW, Lair SV, Thill GP, Siegel RS, Ellis SB;
PI Williams ME;
XX WPI; 1989-165613/22.
DR P-PSDB; AAP92066.
XX Prod. of animal lysozyme C from pinchia pastoris by secretion
XX consists of P. pastoris promoter and terminator DNA
XX for transcription
XX Pages 26-29; 85pp; English.
XX The 3'-noncoding sequence does not contain a polyadenylation signal or a
XX poly (A)+ tail. The 5'-terminus does not contain the ATG triplet
XX corresponding to the translation initiation codon for the pre-lysozyme C2
XX mRNA. Thus the cDNA insert encodes 16 amino acids amino-terminal to the
XX amino-terminus of the mature protein.
SQ Sequence 964 BP; 298 A; 165 C; 200 G; 301 T; 0 other;

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Query Match 98.4%; Score 437; DB 10; Length 964;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-219;  
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 CTCCTGTTATTCCTGGGGTTTCCTTCCTTCTGTCGTCGCAAGGCAAGGCTTTGGA 67
DB 26 CTCCTGTTATTCCTGGGGTTTCCTTCCTTCTGTCGTCGTCGCAAGGCAAGGCTTTGGA 85
QY 68 GATGTGAGCTTGGCCGAAGACTGTGAAGAACTTGGAGCTGAGCGCTATTAAGGAGTCAG 127
DB 86 GATGTGAGCTTGGCCGAAGACTGTGAAGAACTTGGAGCTGAGCGCTATTAAGGAGTCAG 145
QY 128 TGCGCAAACTGTTGTTGTTGACCAATGGGAAGCAAGTTATTAACCAAAAGCTTCAAACT 187
DB 146 TGCGCAAACTGTTGTTGTTGACCAATGGGAAGCAAGTTATTAACCAAAAGCTTCAAACT 205
QY 188 ACAATCTAGACAGTGAAGCACTGATTATGGAATTTTCAGATCAACAGCAATGGTG 247
DB 206 ACAATCTAGACAGTGAAGCACTGATTATGGAATTTTCAGATCAACAGCAATGGTG 265
QY 248 GTAATGATGGCAAAACCCCTAATGAGTGAAGGCTGTCATGTAATCCGCGCAAGTTAA 307
DB 266 GTAATGATGGCAAAACCCCTAATGAGTGAAGGCTGTCATGTAATCCGCGCAAGTTAA 325
QY 308 TGGAAATGACATCGCTTAAGCTGTAGCGTGTGCAAAAGCATATTGTGAGAGCAAGCA 367
DB 326 TGGAAATGACATCGCTTAAGCTGTAGCGTGTGCAAAAGCATATTGTGAGAGCAAGCA 385
QY 368 TTACAGCTGGGTGATGCAAAAGTCTTTGTGAGACCATGACGTGACAGTTACGTTG 427
DB 386 TTACAGCTGGGTGATGCAAAAGTCTTTGTGAGACCATGACGTGACAGTTACGTTG 445
QY 428 AGGGTTGCACCCCTGTA 444
DB 446 AGGGTTGCACCCCTGTA 462

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RESULT 6  
 AAO39092  
 ID AAO39092 standard; DNA; 964 BP.

AC AAO39092;  
 DT 20-JUL-1993 (first entry)

DE Bovine lysozyme c DNA.

XX

KM Bovine; lysozyme c; transgenic; plant; resistance; pathogen;  
 KM gram negative; bacteria; hen egg white lysozyme; potato; tobacco;  
 KM tomato; carrot; apple; sunflower; petunia; violet; pseudomonas;  
 KM Agrobacterium; Xanthomonas; Erwinia; Clavibacter; ss.

```

Db          444  TGAAGGTTGCACCCCTGTAA 462

RESULT 7
ID          AAN70944 standard; DNA; 390 BP.
XX
AC          AAN70944;
XX
DT          09-APR-1991 (first entry)
XX
DE          Sequence encoding mature human lysozyme (HLZ).
XX
KW          Antibacterial; antiviral; bacteriolytic; phagocytosis; ss.
XX
OS          Homo sapiens.
XX
FH          Key
FT          mat_peptide
FT          Location/Qualifiers
FT          1..390
FT          /tag= a
XX
XX          DE3540075-A.
XX          PD          14-MAY-1987.
XX          PF          12-NOV-1985; 85DE-3540075.
XX          PR          12-NOV-1985; 85DE-3540075.
XX          PA          (BOEH ) BOEHRINGER INGELHEI.
XX          PI          Sledziwski A, Chlebowicz-Sledziwska E, Swelly P, Adolf G, Wien AT;
XX          DR          WPI: 1987-136923/20.
XX          DR          P-PSDB; AAP70596.
XX          PT          New hybrid plasmids contg. sequences for human lysozyme - useful
XX          PS          e.g. as antiviral and antibacterial agent, and transformed hosts.
XX          SS          Claim 6; p2; 18pp; German.
XX
CC          A cDNA bank was constructed using total RNA isolated from the human
CC          lymphoma cell line U-937. The bank was tested by hybridising with
CC          two radio-labeled 17-mer oligonucleotides (equiv. to the AA
CC          sequences 26-31 and 63-68 of HLZ). Clones isolated were designated
CC          pHL 14-1; pHL21 and pHL 23 (contg. an approx. 500 bp insert) and
CC          pHL2 and pHL8 (contg. a 300 bp insert).
XX
SQ          Sequence 390 BP; 113 A; 68 C; 113 G; 96 T; 0 other;
XX
Query Match 6.88; Score 30; DB 8; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.0e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
YY          204 AAGCAGCATTTATGGATATTTCAGATCAA 233
XX          |||
XX          150 AAGCAGCATTTATGGATATTTCAGATCAA 179
XX
RESULT 8
ID          AAN92054
XX          AAN92054 standard; DNA; 435 BP.
XX
AC          AAN92054;
XX
DT          07-APR-1990 (first entry)
XX
DE          Sequence of human pre-lysozyme C of placental origin.
XX
KW          Plasmid pHLZ100; human placental pre-lysozyme C; human milk lysozyme;
XX          human histiocyte lymphoma cell line U-937 pre-lysozyme C.
XX
OS          Homo sapiens.
XX

```

```

XX Key Location/Qualifiers
FH conflict replace(36, "T")
FT /*tag= a
FT replace(39, "A")
FT /*tag= b
XX MO8904320-A.
XX 18-MAY-1989.
XX 02-NOV-1988; 88WO-US03907.
XX 02-NOV-1987; 87US-0115940.
XX (SALK ) SALK INST FOR BIOL STUD.
XX Digan ME, Harpold MM, Ialr SV, Thill GP, Siegel RS, Ellis SB;
XX Williams ME;
XX WPI; 1989-165613/22.
XX Prodn. of animal lysozyme C from pichia pastoris by secretion
XX - consists of P. pastoris promoter and terminator DNA
XX for transcription
XX Page 56; ; 85pp; English.
XX Sequence contained in plasmid pHIZ100. Apart from the four N-terminal
XX amino acids, it encodes the entire sequence of human pre-lysozyme C of
XX placental origin in addition to a translational stop signal. The mature
XX lysozyme C corresponding to the pre-lysozyme C encoded by AAN92054 has
XX the same AA sequence as human milk lysozyme. AAN92054 differs from the
XX nucleotide sequence of the cDNAs encoding human pre-lysozyme C isolated
XX from human histiocytic lymphoma cell line U-937 (see FT tags a and b).
XX However, these nucleic acid differences do not alter the amino acid
XX sequence.
XX Sequence 435 BP; 118 A; 79 C; 125 G; 113 T; 0 other;
XX SQ
XX Query Match 6.8%; Score 30; DB 10; Length 435;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-05;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 204 AAGCAGCTATTATGGATTTTCAGATCAA 233
XX 192 AAGCAGCTATTATGGATTTTCAGATCAA 221
XX Db
XX RESULT 9
XX AAD17740
XX ID AAD17740 standard; cDNA; 444 BP.
XX AC AAD17740;
XX XX 10-DEC-2001 (first entry)
XX DE Human macrophage-expressed cDNA #17.
XX XX
XX Human macrophage-expressed protein; inflammation; angiogenesis; cancer;
XX transplantation; myelodysplastic syndrome; transgenic animal; ischaemia;
XX gene therapy; Crohn's disease; immune disorder; myeloid leukaemia; shock;
XX sepsis; nephritis; genetic disorder; nervous system disease; neuropathy;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; fibrosis;
XX amyotrophic lateral sclerosis; lymphoid cell disorder; platelet disorder;
XX thrombocytopenia; osteoarthritis; bone degenerative disorder; thrombosis;
XX periodontal disease; osteoporosis; tissue repair; burn; incision; ulcer;
XX lung; liver; severe combined immunodeficiency; SCID; autoimmune disorder;
XX multiple sclerosis; rheumatoid arthritis; allergy; asthma; thrombolytic;
XX coagulation disorder; hereditary disorder; haemophilia; neuroprotective;
XX antibacterial; immunosuppressive; analgesic; vulnerrary; immunostimulant;
XX vaccine; vasotropic; nootropic; haemostatic; osteopathic; fungicide;
XX antidiabetic; ss.

```

```

XX OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 14..352
FT /*tag= a
FT /*product= "Human macrophage-expressed protein"
FT sig_peptide 14..67
FT /*tag= b
FT mat_peptide 68..349
FT /*tag= c
FT /*product= "Human mature macrophage-expressed protein"
XX WO200164839-A2.
XX 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US06475.
XX 28-FEB-2000; 2000US-0515126.
XX 31-MAR-2000; 2000US-0540217.
XX 11-DEC-2000; 2000US-0235200.
XX (HYSE-) HYSEQ INC.
XX Dedera D, Boyle BJ, Labat I, Strache-crain B, Drmanac RT;
XX Dickson MC, Jones LW, Liu C, Tang YT;
XX WPI; 2001-582152/65.
XX P-PSDB; AAE10592.
XX Novel macrophage-expressed nucleic acids and polypeptides for diagnosis
XX and treatment of inflammatory, autoimmune, neurological, myeloid or
XX lymphoid cell disorders, cancer and for promoting wound healing
XX Claim 1; Page 150; 158pp; English.
XX PS
XX The present invention relates to an isolated macrophage-expressed cDNA
XX and its protein. The invention is used in gene therapy and in creating
XX transgenic animals. Macrophage-expressed molecule is useful treating
XX inflammatory conditions such as nephritis, Crohn's disease, ischaemia-
XX reperfusion injury, shock, sepsis, immune responses, cancer and myeloid
XX leukaemia and myelodysplastic syndromes. The protein exhibits activity
XX relating to angiogenesis, cytokine, stem cell growth factor activity and
XX activating/inhibin related activities and is involved in proliferation,
XX differentiation and survival of pluripotent and totipotent stem cells
XX and useful for re-engineering damaged or diseased tissues, manufacture
XX of bio-pharmaceuticals, development of bio-sensors and transplantation.
XX The protein is used to manipulate stem cells in culture to give rise to
XX neuroepithelial cells that is used to augment or replace cells damaged
XX by illness, accidental damage or genetic disorders, induces the
XX proliferation of neural cells and regeneration of nerve and brain tissue
XX and is useful for the treatment of central and peripheral nervous system
XX diseases and neuropathies, such as Alzheimer's, Parkinson's disease,
XX Huntington's disease, amyotrophic lateral sclerosis and involved in
XX chemotactic or chemokinetic activity, regulation of haematopoiesis and
XX is useful for treating lymphoid cell disorders, platelet disorders such
XX as thrombocytopenia and osteoporosis, osteoarthritis, bone degenerative
XX disorders or periodontal disease and for regeneration of bone, cartilage,
XX tendon and ligament and in tissue repair, healing of burns, incisions
XX and ulcers. The invention is also useful for gut protection, treatment
XX of lung or liver fibrosis, immune deficiencies and disorders such as
XX severe combined immunodeficiency (SCID), bacterial or fungal infections,
XX autoimmune disorders eg. multiple sclerosis, rheumatoid arthritis,
XX allergies such as asthma or other respiratory problems and is involved
XX in thrombolytic or thrombotic or other respiratory problems and is involved
XX in coagulation (hereditary disorders such as haemophilia) or to enhance
XX coagulation and other haemostatic events in treating wounds resulting
XX from trauma, surgery and inhibits the growth, effects biorhythms or
XX circadian cycles of rhythms, fertility of male or female subjects,
XX metabolism, catabolism, anabolism, processing utilisation, storage or
XX elimination of dietary fat, lipid, protein, carbohydrate, vitamins,
XX minerals, provides analgesic effects or other pain reducing effects,
XX

```

CC Immunoglobulin like activity and as an antigen in a vaccine composition  
CC to raise an immune response. The present sequence is human macrophage-  
CC expressed cDNA.

XX Sequence 444 BP; 122 A; 92 C; 121 G; 109 T; 0 other;

Query Match 6.8%; Score 30; DB 22; Length 444;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233  
Db 217 AAGCACTGATTATGGATATTTTCAGATCAA 246

RESULT 10  
ID AAN70943 standard; DNA; 447 BP.

XX AAN70943;

XX 09-APR-1991 (first entry)

DE Sequence encoding leader or signal peptide and mature human  
DE lysozyme (HLZ).

XX Antibacterial; antiviral; bacteriolytic; phagocytosis; ss.

XX Homo sapiens.

FT Key Location/Qualifiers

FT met-peptide 43..432

FT /\*tag- a

PN DE3540075-A.

XX 14-MAY-1987.

PF 12-NOV-1985; 85DE-3540075.

XX 12-NOV-1985; 85DE-3540075.

PA (BOEH ) BOEHRINGER INGELHEIM.

PI Siedzlewski A, Chlebowicz-Siedzewska E, Swelly P, Adolf G, Wien AT;

DR WPI; 1987-136923/20.

DR P-PSDB; AAP70596.

XX New hybrid plasmids contg. sequences for human lysozyme - useful

PT e.g. as antiviral and antibacterial agent, and transformed hosts.

XX Claim 5; p2; 18pp; German.

CC A cDNA bank was constructed using total RNA isolated from the human

CC lymphoma cell line U-937. The bank was tested by hybridising with

CC two radio-labeled 17-mer oligonucleotides (equiv. to the AA

CC sequences 26-31 and 63-68 of HLZ). Clones isolated were designated

CC PHL14-1; PHL21 and PHL 23 (contg. an approx. 500 bp insert) and

CC PHL2 and PHL8 (contg. a 300 bp insert).

SQ Sequence 447 BP; 122 A; 81 C; 125 G; 119 T; 0 other;

RESULT 11

ABL37496  
ID ABL37496 standard; CDNA; 481 BP.

XX ABL37496;

XX 08-APR-2002 (first entry)

DE Human colon tumour antigen polynucleotide SEQ ID NO:1085.

XX Human; colon cancer; colon tumour antigen; cytostatic; vaccine;

XX colon tumour metastatic antigen; diagnosis; gene; ss.

XX Homo sapiens.

PN WO200196388-A2.

XX 20-DEC-2001.

XX 08-JUN-2001; 2001WO-US18557.

XX 09-JUN-2000; 2000US-210899P.

XX 20-FEB-2001; 2001US-270216P.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Harlocker SL, Secrist H;

XX WPI; 2002-114514/15.

XX Novel isolated colon tumor polynucleotide differentially expressed in

XX colon tumor or colon metastatic tumor and polypeptides encoded by them,

XX useful for inhibiting development of cancer in patient -

XX Claim 1; SEQ ID 1085; 105pp; English.

XX ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)

XX CC which were isolated from human colon tumour and colon metastatic tumour

XX CC cDNA libraries. (I) have cytosolic activity and can be used in vaccine

XX CC production. (I) can be used for stimulating and/or expanding T cells

XX CC specific for a tumour protein on contact with the T cells. They are also

XX CC useful for inhibiting the development of cancer in a patient. (I) can be

XX CC used as probes or primers for nucleic acid hybridisation, for preparing

XX CC mutant species primers, or primers for use in genetic constructions. (I)

XX CC can be used in the diagnosis of a colon tumour.

SQ Sequence 481 BP; 127 A; 93 C; 128 G; 131 T; 2 other;

Query Match 6.8%; Score 30; DB 24; Length 481;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233

Db 189 AAGCACTGATTATGGATATTTTCAGATCAA 218

RESULT 12  
ID AAN70949 standard; CDNA; 490 BP.

XX AAN70949;

XX 09-APR-1991 (first entry)

DE Sequence encoding human lysozyme (HLZ) on cDNA clone HL14-1.

XX Antibacterial; antiviral; bacteriolytic; phagocytosis; ss.

XX Homo sapiens.

FT Key Location/Qualifiers

FT CDS 19..454

FT /\*tag- a

XX DE3540075-A.  
 XX  
 XX 14-MAY-1987.  
 XX  
 XX 12-NOV-1985; 85DE-3540075.  
 XX  
 XX 12-NOV-1985; 85DE-3540075.  
 XX  
 XX (BOEH ) BOEHRINGER INGELHEI.  
 XX  
 XX Siedzielski A, Chlebowski-Siedzielska E, Swelly P, Adolf G, Wien AT;  
 XX  
 XX WPI; 1987-136923/20.  
 XX  
 XX P-PSDB; AAP70599.  
 XX  
 XX New hybrid plasmids contg. sequences for human lysozyme - useful  
 XX e.g. as antiviral and antibacterial agent, and transformed hosts.  
 XX  
 XX PS Disclosure; Fig 4; 18pp; German.  
 XX  
 XX A cDNA bank was constructed using total RNA isolated from the human  
 XX lymphoma cell line U-937. The bank was tested by hybridising with  
 XX two radio-labeled 17-mer oligonucleotides (equiv. to the AA  
 XX sequences 26-31 and 63-68 of HLZ). Clones isolated were designated  
 XX pH14-1, pH21 and pH23 (contg. an approx. 500 bp insert) and  
 XX pH2 and pH8 (contg. a 300 bp insert).  
 XX  
 XX SQ Sequence 490 BP; 122 A; 100 C; 149 G; 119 T; 0 other;  
 OY  
 Query Match 6.8%; Score 30; DB 8; Length 490;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 204 AACGACTGATTTATGGATATTTTCAGATCAA 233  
 ||||||||||||||||||||||||||||  
 211 AACGACTGATTTATGGATATTTTCAGATCAA 240  
 Db  
 RESULT 13  
 ABL38017/c  
 ID ABL38017 standard; cDNA; 585 BP.  
 XX  
 XX ABL38017;  
 AC  
 XX 08-APR-2002 (first entry)  
 DT  
 XX Human colon tumour antigen polynucleotide SEQ ID NO:1606.  
 DE  
 XX Human; colon cancer; colon tumour antigen; cytostatic; vaccine;  
 KM colon tumour metastatic antigen; diagnosis; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200196388-A2.  
 XX  
 XX PD 20-DEC-2001.  
 XX  
 XX PF 08-JUN-2001; 2001WO-US18557.  
 XX  
 XX PR 09-JUN-2000; 2000US-210899P.  
 XX  
 XX PR 20-FEB-2001; 2001US-270216P.  
 XX  
 XX PA (CORI-) CORIXA CORP.  
 XX  
 XX PI Jiang Y, Harlocker SL, Secrist H;  
 XX  
 XX DR WPI; 2002-114514/15.  
 XX  
 XX Novel isolated colon tumor polynucleotide differentially expressed in  
 XX colon tumor or colon metastatic tumor and polypeptides encoded by them,  
 XX useful for inhibiting development of cancer in patient -

PS Claim 1; SEQ ID 1606; 105pp; English.  
 XX  
 XX ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)  
 XX which were isolated from human colon tumour and colon metastatic tumour  
 XX cDNA libraries. (I) have cytostatic activity and can be used in vaccine  
 XX production. (I) can be used for stimulating and/or expanding T cells  
 XX specific for a tumour protein on contact with the T cells. They are also  
 XX useful for inhibiting the development of cancer in a patient. (I) can be  
 XX used as probes or primers for nucleic acid hybridisation, for preparing  
 XX mutant species primers, or primers for use in genetic constructions. (I)  
 XX can be used in the diagnosis of a colon tumour.  
 XX  
 XX SQ Sequence 585 BP; 173 A; 123 C; 108 G; 179 T; 2 other;  
 OY  
 Query Match 6.8%; Score 30; DB 24; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 204 AACGACTGATTTATGGATATTTTCAGATCAA 233  
 ||||||||||||||||||||||||||||  
 511 AACGACTGATTTATGGATATTTTCAGATCAA 482  
 Db  
 RESULT 14  
 AAA16339  
 ID AAA16339 standard; DNA; 657 BP.  
 XX  
 XX AAA16339;  
 AC  
 XX 14-JUN-2000 (first entry)  
 DT  
 XX Human colon cancer differentially expressed nucleotide sequence #344.  
 DE  
 XX Human colon cancer; detect; differential expression; human; treatment;  
 KM detect mutation; non-invasive diagnostic method; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200012702-A2.  
 XX  
 XX PD 09-MAR-2000.  
 XX  
 XX PF 30-AUG-1999; 99WO-US19424.  
 XX  
 XX PR 31-AUG-1998; 98US-0098639.  
 XX  
 XX PR 27-JAN-1999; 99US-0117393.  
 XX  
 XX PA (FARB ) BAYER CORP.  
 XX  
 XX Endege WO, Steilmann KE, Astle JH, Burgess CC, Carroll E;  
 XX Catino TJ, Dwyer P, Ford DM, Lewis ME, Molino GA, Monahan JE;  
 XX Schlegel R;  
 XX  
 XX DR WPI; 2000-256641/22.  
 XX  
 XX Novel nucleic acids and proteins for identifying therapeutic agents  
 XX useful for treating and diagnosing cancer, especially colon cancer -  
 XX  
 XX PS Claim 16; Page 263; 345pp; English.  
 XX  
 XX This sequence represents a human nucleotide sequence which is  
 XX differentially expressed in colon cancer cells compared to the expression  
 XX levels in normal cells. The nucleotide sequence can be used as a source  
 XX of primers and probes. The nucleotide sequence is useful for determining  
 XX the phenotype of a cell by detecting the differential expression of the  
 XX sequence relative to a normal cell. The probes derived from the sequence  
 XX can also be used to determine the phenotype of cells in a sample. Probes  
 XX used to determine the phenotype of a cell. The primers are useful for  
 XX detecting a mutation in a test nucleotide sequence and also for detecting  
 XX cancer, preferably colon cancer. Antibodies against the protein encoded  
 XX by the nucleotide sequence can also be used in a method to detect colon  
 XX cancer. The diagnostic method is non-invasive and accurate for diagnosing

CC colon cancer at an early stage.  
 XX  
 SQ Sequence 657 BP; 184 A; 122 C; 158 G; 178 T; 15 other;

Query Match 6.8%; Score 30; DB 21; Length 657;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGATATTCAGATCAA 233  
 Db 205 AAGCACTGATTATGATATTCAGATCAA 234

Db 516 AAGCACTGATTATGATATTCAGATCAA 487

Search completed: July 5, 2003, 06:20:13  
 Job time : 182 secs

RESULT 15  
 ID ABO58989/c  
 XX ABO58989 standard; cDNA; 706 BP.

AC ABO58989;

DT 02-AUG-2002 (first entry)

DE Human colon cancer related nucleotide sequence SEQ ID NO:2684.

KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;  
 genetic analysis; diagnostic; antisense therapy; gene; ss.

OS Homo sapiens.

PN WO200229086-A2.

PD 11-APR-2002.

PF 02-OCT-2001; 2001WO-US30732.

PR 02-OCT-2000; 2000US-237271P.

PA (PARB ) BAYER CORP.

PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;  
 PI Thiagalingam A, Lewis ME;

DR WPI; 2002-426115/45.

PT New isolated nucleic acid that is differentially expressed in cancer  
 PT tissues useful for determining the presence of colon cancer in a cell  
 or tissue type, and in antisense therapy

PS Claim 1; Fig 1; 796pp; English.

CC ABO56306 to ABO60787 represent isolated nucleic acids (I) differentially  
 CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins  
 CC encoded by the ABO60776 to ABO60787 nucleic acid sequences. (I) can be  
 CC used in antisense therapy. An antibody immunoreactive with a polypeptide  
 CC encoded by (I) is useful for detecting cancer in a patient sample, and  
 CC for detecting the presence or absence of a polynucleotide encoded by a  
 CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived  
 CC from (I) can be used for determining the presence of a nucleic acid which  
 CC hybridizes to (I), and for determining the phenotype of cells in a sample  
 CC of cells from a patient. (I) is useful for determining the presence of  
 CC colon cancer in a cell or tissue type, for determining the presence or  
 CC state of other type of cancer, in antisense therapy, to generate  
 CC microarrays on a solid surface, to identify a chromosome on which the  
 CC corresponding gene resides, and in tissue profiling, forensics, genetic  
 CC analysis, mapping, and diagnostic applications. (I) can be used to raise  
 CC antibodies, and to screen for peptide analogues and antagonists.

SQ Sequence 706 BP; 196 A; 156 C; 134 G; 206 T; 14 other;

Query Match 6.8%; Score 30; DB 24; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGATATTCAGATCAA 233



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 05:50:38 ; Search time 1138 Seconds  
(without alignments)  
6318.802 Million cell updates/sec

Title: US-09-978-199-1

Perfect score: 444  
Sequence: 1 atgaagctctcgttatctcttgcacccctgtaa 444

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_hiv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	444	100.0	453	BG937925	BG937925 1AB009H04
2	444	100.0	462	BG938107	BG938107 1AB011D05
3	444	100.0	463	BG938377	BG938377 1AB016E03
4	444	100.0	464	BG938413	BG938413 1AB007G10
5	444	100.0	469	BG938112	BG938112 1AB011D12
6	444	100.0	476	BG937589	BG937589 1AB003C3

7	444	100.0	476	13	BG938203	BG938203 1AB013G08
8	444	100.0	478	13	BG937601	BG937601 1AB003H1
9	444	100.0	481	13	BG937832	BG937832 1AB007G03
10	444	100.0	482	13	BG937936	BG937936 1AB008E01
11	444	100.0	484	13	BG937881	BG937881 1AB009C06
12	444	100.0	485	13	BG938200	BG938200 1AB013G04
13	444	100.0	486	13	BG937882	BG937882 1AB009C07
14	444	100.0	487	13	BG938101	BG938101 1AB011C10
15	444	100.0	487	13	BG938250	BG938250 1AB014E01
16	444	100.0	491	13	BG937866	BG937866 1AB009A09
17	444	100.0	493	13	BG937861	BG937861 1AB009A04
18	444	100.0	494	13	BG938345	BG938345 1AB016A01
19	444	100.0	497	13	BG937747	BG937747 1AB006A06
20	444	100.0	497	13	BG938042	BG938042 1AB012E07
21	444	100.0	498	13	BG937670	BG937670 1AB004G05
22	444	100.0	502	13	BG937865	BG937865 1AB009A08
23	444	100.0	503	13	BG937991	BG937991 1AB010H03
24	444	100.0	513	13	BG938316	BG938316 1AB015E06
25	444	100.0	525	10	AM654651	AM654651 10A668 MA
26	444	99.8	448	13	BG937749	BG937749 1AB006A09
27	439	98.9	448	13	BG938303	BG938303 1AB015C05
28	439	98.9	484	13	BG938144	BG938144 1AB008E07
29	438	98.6	453	13	BG937445	BG937445 1AB001E04
30	437	98.4	456	13	BG938205	BG938205 1AB013G10
31	432	97.3	448	13	BG937811	BG937811 1AB007D02
32	432	97.3	450	13	BG938187	BG938187 1AB013E09
33	431	97.1	453	13	BG937415	BG937415 1AB001A08
34	430	96.8	438	13	BG937513	BG937513 1AB002H02
35	430	96.8	446	13	BG937575	BG937575 1AB003A6
36	429	96.6	446	13	BG937679	BG937679 1AB004H07
37	429	96.6	447	13	BG937658	BG937658 1AB004E08
38	429	96.6	453	13	BG937506	BG937506 1AB002G01
39	429	96.6	465	13	BG937509	BG937509 1AB002G04
40	428	96.4	438	13	BG937696	BG937696 1AB005D04
41	428	96.4	442	13	BG937577	BG937577 1AB003C6
42	428	96.4	442	13	BG938191	BG938191 1AB013F01
43	428	96.4	443	13	BG937880	BG937880 1AB009C05
44	428	96.4	445	13	BG938335	BG938335 1AB015G08
45	428	96.4	454	13	BG938097	BG938097 1AB011C03

## ALIGNMENTS

RESULT 1  
LOCUS BG937925 453 bp mRNA linear EST 11-JUN-2001  
DEFINITION 1AB009H04 Bovine Abomasum cDNA Library Bos taurus CDNA 5', mRNA  
ACCESSION BG937925  
VERSION BG937925.1 GI:14337297  
KEYWORDS EST.  
SOURCE COW.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 453)  
Moore S.S., Hansen C., Li C., Fu A., Meng Y. and Li G.  
CDNA's from bovine abomasum tissue  
Unpublished (2001)  
CONTACT: Dr. Stephen Moore  
Beef Genomics Laboratory  
Dept of AFNS, University of Alberta  
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0169  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
The sequence best matches gb:BovLZYMTA (Bos taurus lyszyme 7A mRNA  
) in main database at high score of 898.0 and E-value of 0.0  
PCR PRIMERS  
FORWARD: M13 Forward  
BACKWARD: M13 Reverse



KEYWORDS	EST.
SOURCE	COW.
ORGANISM	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
AUTHORS	Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
TITLE	CDNA 5' from bovine abomasum tissue
JOURNAL	Unpublished (2001)
COMMENT	Contact: Dr. Stephen Moore Dept of AFNS, University of Alberta 410 Agr./For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169 Fax: 780 492 4265 Email: smoores@afns.ualberta.ca (The sequence best matches gb:BOV12YM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 918.0 and E-value of 0.0)
PCR primers	PCR primers
FORWARD: M13 Forward	
BACKWARD: M13 Reverse	
Seq primer: T3 primer	
High quality sequence stop: 463	
POLYA-No	
FEATURES	Location/Qualifiers
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	/db_xref="taxon:9913"
	/clone_lib="Bovine Abomasum cDNA Library"
	/sex="Two males and one female mixed"
	/tissue_type="Gastrointestinal tissue (GIT)"
	/cell_type="Epithelial"
	/dev_stage="Young adult"
	/lab_host="X11-BluemRF"-strain"
	/note="Organ: Abomasum; Vector: Uni-Z2APXR; Site_1: Ecor I; Site_2: Xho I"
BASE COUNT	133 a 91 c 119 g 120 t
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Best Local Similarity	100.0%; Pred. No. 1.5e-223;
Matches 444;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAAGGCTCTGTTATTCGTGGGTTTCCTTCCTTCCTTCGTGCGCTGCCAAGCAAGGTC	60
20 ATGAAGGCTCTGTTATTCGTGGGTTTCCTTCCTTCCTTCGTGCGCTGCCAAGCAAGGTC	79
61 TTTGAGAGATGTGAGCTTCCAGAACTGAAAGAACTTGAGAACTTGAGAGAGGCTATTAAGGA	120
80 TTTGAGAGATGTGAGCTTCCAGAACTGAAAGAACTTGAGAGAGGCTATTAAGGA	139
121 GTGAGCCCTGGCAACTGGTTGTTGTTGACCAATGGAAGCAAGTATTAACACAAAGCT	180
140 GTGAGCCCTGGCAACTGGTTGTTGTTGACCAATGGAAGCAAGTATTAACACAAAGCT	199
181 ACAAACTACAATCTCTAGCAGTGAAGCACTGATTATGGGATATTTACATCAACAGCAAA	240
200 ACAAACTACAATCTCTAGCAGTGAAGCACTGATTATGGGATATTTACATCAACAGCAAA	259
241 TGGTGGTATATGATGAGCAAAACCCCTATGACAGTGTGACGGCTGTCATGATCTCCGACG	300
260 TGGTGGTATATGATGAGCAAAACCCCTATGACAGTGTGACGGCTGTCATGATCTCCGACG	319
301 GAATTAATGAAAAATGACATGCGCTTAAGCTGTAGAGGTGCAAAAGCATATTGTGAGTAG	360
320 GAATTAATGAAAAATGACATGCGCTTAAGCTGTAGAGGTGCAAAAGCATATTGTGAGTAG	379
361 CAAGGCATTAACAGCTTGGGTGGCATGAAAAAGTCATTGTCGAGACCATGAGCTCAGCAGT	420
380 CAAGGCATTAACAGCTTGGGTGGCATGAAAAAGTCATTGTCGAGACCATGAGCTCAGCAGT	439
421 TAGCTTGAAGGTTGCACCCCTGTAA 444	

Db	440	TAGCTTGAGGGTTGCACCCCTGTAA	463
RESULT 4			
BG38413			
LOCUS			
DEFINITION	1ab007G10	Bovine Abomasum cDNA Library	Bos taurus cDNA 5', mRNA
ACCESSION			
VERSION	BG38413.1	GI:14337785	
KEYWORDS	EST.		
SOURCE			
ORGANISM			
	Bos taurus		
	Eulazpota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
	Bovidae; Bovinae; Bos.		
	1 (bases 1 to 464)		
	Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y., and Li, G.		
	cDNA's from bovine abomasum tissue		
	unpublished (2001)		
	Contact: Dr. Stephen Moore		
	. Beef Genomics Laboratory		
	Dept of AFNS, University of Alberta		
	410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada		
	Tel: 780 492 0159		
	Fax: 780 492 4265		
	Email: smoores@atns.ualberta.ca		
	The sequence best matches gb:BOVIZYM7A (Bos taurus lysozyme 7A mRNA		
	) in main database at high score of 920.0 and E-value of 0.0		
	PCR primers		
	FORWARD: M13 Forward		
	BACKWARD: M13 Reverse		
	Seq primer: T3 primer		
	POLYA-No.		
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	Location/Qualifiers		
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	/db_xref="taxon:9913"		
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	/tissue_type="Gastrointestinal tissue (GIT)"		
	/cell_type="Epithelial"		
	/dev_stage="Young adult"		
	/lab_host="XL1-BlueMRF", strain"		
	/note="Organ: Abomasum; Vector: Uni-Z2APX; Site_1: EcoR		
	I; Site_2: Xho I"		
BASE COUNT	132 a	92 c	121 g 119 t
ORIGIN			
Query Match	100.0%;	Score 444;	DB 13; Length 464;
Best Local Similarity	100.0%;	Pred. No. 1.5e-223;	
Matches 444;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGAAGGCTCCTGATATCTGGGGTTCTTCCTTCCTGTCGCTGCAAGCAAGGTC	60
DB	14	ATGAAGGCTCCTGATATCTGGGGTTCTTCCTTCCTGTCGCTGCAAGCAAGGTC	73
QY	61	TTTGAGAGTGTGACCTTGCCAGAACTGGAAGAACTGGAAGGCTTAAGGA	120
DB	74	TTTGAGAGTGTGACCTTGCCAGAACTGGAAGAACTGGAAGGCTTAAGGA	133
QY	121	GTGAGCTGGCAAACTGGTGTGTTGTAACCAATGGAAGAGCAATTATACCAAAAGCT	180
DB	134	GTGAGCTGGCAAACTGGTGTGTTGTAACCAATGGAAGAGCAATTATACCAAAAGCT	193
QY	181	ACAACTCAATCCCTAGAGAGTGAAGCACTGATTTGGATTTTCAGATCAACAGCAA	240
DB	194	ACAACTCAATCCCTAGAGAGTGAAGCACTGATTTGGATTTTCAGATCAACAGCAA	253
QY	241	TGCTGTGTAATGATGAGCAAAACCCCTATGAGAGTGAAGGCTCATGATATCTGACGC	300
DB	254	TGCTGTGTAATGATGAGCAAAACCCCTATGAGAGTGAAGGCTCATGATATCTGACGC	313

QY	301	GAATTAAATGGAAAAAGACATGCGTAACCGTAGCGTGCMAAGCATATTGTCAGTAG	360
Db	314	GAATTAAATGGAAAAAGACATGCGTAACCGTAGCGTGCMAAGCATATTGTCAGTAG	373
QY	361	CAAGCATTAACAGCCGCGGTGGCATGAGAAAGTATTGTGAGACCATGACGTCAAGCAT	420
Db	374	CAAGCATTAACAGCCGCGGTGGCATGAGAAAGTATTGTGAGACCATGACGTCAAGCAT	433
QY	421	TACGTTGAGGGTTGGCACCCCTGTAA	444
Db	434	TACGTTGAGGGTTGGCACCCCTGTAA	457

REFERENCE	1 (bases 1 to 469)
AUTHORS	Moore,S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
TITLE	CDNA's from bovine abomasum tissue
JOURNAL	Unpublished (2001)
COMMENT	Contact: Dr. Stephen Moore

Dept of AFNS, University of Alberta  
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0165  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
The sequence best matches gb:BOYLZVW7A (Bos taurus lysozyme 7A mRNA)  
) in main database at high score of 930.0 and E-value of 0.0  
PCR Primers  
FORWARD: M13 Forward  
BACKWARD: M13 Reverse  
Seq primer: T3 primer  
High quality sequence stop: 469  
POLYA-No.

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1..469	/organism="Bos taurus"
	/db_xref="taxon.9913"
	/clone_lib="Bovine Abomasum cDNA Library"
	/sex="Two males and one female mixed"
	/tissue_type="Gastrointestinal tissue (GIT)"
	/cell_type="Epithelial"
	/dev_stage="Young adult"
	/lab_host="X11-BlueMR"-strain"
	/note="Organ: Abomasum; Vector: Uni-ZAPPR; Site_1: Ecor
	I; Site_2: Xho I"
133 a	92 c 123 g 121 t

Query Match:	100.0%;	Score 444;	DB 13;	Length 469;
Best local Similarity	100.0%;	Pred. No. 1.5e-223;		
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAGCCTCGATTATCTGTGGGGTTCCTCTTCTGTCGCGTCCAGGCAAGGTC	60	
Db	17	ATGAAGGCTCTCGATTATCTGTGGGGTTCCTCTTCTGTCGCGTCCAGGCAAGGTC	76	
QY	61	TTTGAGACATGTGAGCTTGGCAGACCTCTAAGAACTGGACTGGAGCGATATAGGA	120	
Db	77	TTTGAGACATGTGAGCTTGGCAGACCTCTAAGAACTGGACTGGAGCGCTATATAGGA	136	

QY	121	GTAGCGTGGCAAACTGGTGTGGTTTGACCAAAATGGGAAACACTGTATTAACAAAAAGCT	180
Db	137	GTAGCGCTGGCAAACTGGTGTGGTTTGACCAAAATGGGAAACACTTTTAAACAAAAGCT	196
QY	181	ACAACATCAATCCTAGCAGTAAGACACTGATTAATGGGATATTTTCAGATCAACAGCANA	240
Db	197	ACAACATCAATCCTAGCAGTGAAGACACTGATTAATGGGATATTTTCAGATCAACAGGANA	256
QY	241	TGTTGGTGTATATGATATGGCAAAAACCCCTAATGCACTGTGACGGCTGTCAATGATCCTGCAGC	300
Db	257	TGTTGGTGTATATGATATGGCAAAAACCCCTAATGCACTGTGACGGCTGTCAATGATCCTGCAGC	316
QY	301	GAATTATATGAAAATATGACATGCTTAACCTGAGCGTGTGCAAAAGCATATTTGCATGAGAG	360
Db	317	GAATTATATGAAAATATGACATGCTTAACCTGAGCGTGTGCAAAAGCATATTTGCATGAGAG	376
QY	361	CAAGGCAATTACAGCCTGGGTGGCAGTAAGAAAGTCAATGTGCAGACATGAGCAGTCAACAGT	420
Db	377	CAAGGCAATTACAGCCTGGGTGGCAGTAAGAAAGTCAATGTGCAGACATGAGCAGTCAACAGT	436
QY	421	TACGTTGAGGGTTGCACCCCTGTAA	444
Db	437	TACGTTGAGGGTTGCACCCCTGTAA	460

RESULT 6	BG937589	476 bp	mRNA	linear	EST 11-JUN-2001
LOCUS	BG937589				
DEFINITION	BG937589	1AB003C3	Bovine Abomasum	CDNA Library	Bos taurus CDNA 5', mRNA
ACCESSION	BG937589	sequence.			
VERSION	BG937589				
KEYWORDS	BG937589.1	GI:14336961			
SOURCE	EST.				
ORGANISM	COW.				
	Bos taurus				

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Moore, S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.  
CDNA's from bovine abdominal tissue  
Unpublished (2001)  
Contact: Dr. Stephen Moore

1 (bases 1 to 476)  
Bovidae; Bovinae; Bos.  
Eukaryota; Metazoa; Chordata; Crinata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae; Bovinae; Bos.

Dept of AFNS, University of Alberta  
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0165  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
The sequence best matches gb:BOVLYZW7A (Bos taurus lysozyme 7A mRNA), in main database at high score of 944.0 and E-value of 0.0  
PCR Primers  
FORWARD: M13 Forward  
BACKWARD: M13 Reverse  
Seq primer: T3 primer  
High quality sequence stop: 476  
POLYA-NO.

FEATURES	Location/Qualifiers
source	1..476
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	/tissue_type="Gastrointestinal tissue (GIT)"
	/cell_type="Epithelial"
	/dev_stage="Young adult"
	/lab_host="X11-BiueMRF"-strain"
	/note="Organ: Abomasum; Vector: Uni-ZAPPR; Site_1: EcoR I; Site_2: Xho I"
BASE COUNT	135 a 94 c 122 g 125 t
ORIGIN	
Query Match	100.0%; Score 444; DB 13; Length 476;

Best Local Similarity 100.0%; Pred. No. 1.5e-223;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTGCTTATTCCTGGGGTTCCTTCTTCTGCTCTCCAGGCAAGGTC 60  
DB 6 ATGAAGGCTCTGCTTATTCCTGGGGTTCCTTCTTCTGCTCTCCAGGCAAGGTC 65  
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DB 66 TTGAGAGATGTAGCTTGCACAACTGTGAAGAACTTGAGCTGACGGCTTAAGGA 125  
QY 121 GTACGCTGGCAAACTGCTGTTGTTGACCAAAATGGGAAAGCAATTATTAACAAAAGCT 180  
DB 126 GTACGCTGGCAAACTGCTGTTGTTGACCAAAATGGGAAAGCAATTATTAACAAAAGCT 185  
QY 181 ACAAGCTCAATCTGAGCTGGAAGCACTGATTAGGATATTTAGATCAACACAAA 240  
DB 186 ACAAGCTCAATCTGAGCTGGAAGCACTGATTAGGATATTTAGATCAACACAAA 245  
QY 241 TGGTGTGTAATGATGCAAAACCCCTAATGCAAGGCTGTGATGATCTGACG 300  
DB 246 TGGTGTGTAATGATGCAAAACCCCTAATGCAAGGCTGTGATGATCTGACG 305  
QY 301 GAATTATGAAAAATGACATCGCTTAAGCTGTGAGCTGTGCAAAAGCATATTGTCACTGAG 360  
DB 306 GAATTATGAAAAATGACATCGCTTAAGCTGTGAGCTGTGCAAAAGCATATTGTCACTGAG 365  
QY 361 CAAGGCTTACAGCTGGGTGGCAAGAAAGTCATTGTGAGACATGACGTCACAGCT 420  
DB 366 CAAGGCTTACAGCTGGGTGGCAAGAAAGTCATTGTGAGACATGACGTCACAGCT 425  
QY 421 TACGTTGAGGGTTGCACCCCTGTA 444  
DB 426 TACGTTGAGGGTTGCACCCCTGTA 449

RESULT 7  
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LOCUS 1Ab013G08 Bovine Abomasum cDNA Library Bos taurus CDNA 5', mRNA  
DEFINITION  
ACCESSION BG938203  
VERSION BG938203.1 GI:14337575  
KEYWORDS EST.  
SOURCE  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE  
AUTHORS Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.  
TITLE CDNA's from bovine abomasum tissue  
JOURNAL Unpublished (2001)  
COMMENT Contact: Dr. Stephen Moore  
Beef Genomics Laboratory  
Dept of AFNS, University of Alberta  
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0169  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
The sequence best matches gb:BOVL2YM7A (Bos taurus lysozyme 7A mRNA  
) in main database at high score of 944.0 and E-value of 0.0

FEATURES  
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/organism="Bos taurus"  
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/sex="Two males and one female mixed"  
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/cell\_type="Epithelial"  
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BASE COUNT 135 a 93 c 123 g 125 t

ORIGIN

Query Match 100.0%; Score 444; DB 13; Length 476;  
Best Local Similarity 100.0%; Pred. No. 1.5e-223;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGCTCTGCTTATTCCTGGGGTTCCTTCTTCTGCTCTCCAGGCAAGGTC 60  
DB 18 ATGAAGGCTCTGCTTATTCCTGGGGTTCCTTCTTCTGCTCTCCAGGCAAGGTC 77  
QY 61 TTGAGAGATGTAGCTTGCACAACTGTGAAGAACTTGAGCTGACGGCTTAAGGA 120  
DB 78 TTGAGAGATGTAGCTTGCACAACTGTGAAGAACTTGAGCTGACGGCTTAAGGA 137  
QY 121 GTACGCTGGCAAACTGCTGTTGTTGACCAAAATGGGAAAGCAATTATTAACAAAAGCT 180  
DB 138 GTACGCTGGCAAACTGCTGTTGTTGACCAAAATGGGAAAGCAATTATTAACAAAAGCT 197  
QY 181 ACAAGCTCAATCTGAGCTGGAAGCACTGATTAGGATATTTAGATCAACACAAA 240  
DB 198 ACAAGCTCAATCTGAGCTGGAAGCACTGATTAGGATATTTAGATCAACACAAA 257  
QY 241 TGGTGTGTAATGATGCAAAACCCCTAATGCAAGGCTGTGATGATCTGACG 300  
DB 258 TGGTGTGTAATGATGCAAAACCCCTAATGCAAGGCTGTGATGATCTGACG 317  
QY 301 GAATTATGAAAAATGACATCGCTTAAGCTGTGAGCTGTGCAAAAGCATATTGTCACTGAG 360  
DB 318 GAATTATGAAAAATGACATCGCTTAAGCTGTGAGCTGTGCAAAAGCATATTGTCACTGAG 377  
QY 361 CAAGGCTTACAGCTGGGTGGCAAGAAAGTCATTGTGAGACATGACGTCACAGCT 420  
DB 378 CAAGGCTTACAGCTGGGTGGCAAGAAAGTCATTGTGAGACATGACGTCACAGCT 437  
QY 421 TACGTTGAGGGTTGCACCCCTGTA 444  
DB 438 TACGTTGAGGGTTGCACCCCTGTA 461

RESULT 8  
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LOCUS 1Ab0303H1 Bovine Abomasum cDNA Library Bos taurus CDNA 5', mRNA  
DEFINITION  
ACCESSION BG937601  
VERSION BG937601.1 GI:14336973  
KEYWORDS EST.  
SOURCE  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE  
AUTHORS Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.  
TITLE CDNA's from bovine abomasum tissue  
JOURNAL Unpublished (2001)  
COMMENT Contact: Dr. Stephen Moore  
Beef Genomics Laboratory  
Dept of AFNS, University of Alberta  
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0169  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
The sequence best matches gb:BOVL2YM7A (Bos taurus lysozyme 7A mRNA  
) in main database at high score of 948.0 and E-value of 0.0



sequence.  
 accession BG937936  
 version BG937936.1 GI:14337308  
 keywords EST.  
 source cow.  
 organism Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 482)  
 Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.  
 CDNA's from bovine abomasum tissue  
 unpublished (2001)  
 contact: Dr. Stephen Moore  
 Beef Genomics Laboratory  
 Dept of AFNS, University of Alberta  
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 Tel: 780 492 0169  
 Fax: 780 492 4265  
 Email: smoores@afns.ualberta.ca  
 The sequence best matches gb:BOVLZYMTA (Bos taurus lysozyme 7A mRNA  
 ) in main database at high score of 955.0 and E-value of 0.0  
 PCR Primers  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 482  
 POLYA-No.  
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 /dev\_stage="Young adult"  
 /lab\_host="XLI-BlueMRF"-strain"  
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 I; Site\_2: Xho I"  
 BASE COUNT 136 a 96 c 123 g 127 t  
 ORIGIN  
 Query Match 100.0%; Score 444; DB 13; Length 482;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-223;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ATGAAGGCTCTGCTATTCCTGGGGTTCCTCTTCTGCGCTGCCAAGCAAGTTC 60  
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 12 ATGAAGGCTCTGCTATTCCTGGGGTTCCTCTTCTGCGCTGCCAAGCAAGTTC 71  
 |||||  
 61 TTGAGAGATGTGAGTTGGCTGCAAGTGAAGAACTTGGAGCGCTATTAAGGA 120  
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 72 TTGAGAGATGTGAGTTGGCTGCAAGTGAAGAACTTGGAGCGCTATTAAGGA 131  
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 121 GTCAGCGCTGGCAAACTGTTGTTGTGACCAATGGGAAAGCAAGTATAACAAAGCT 180  
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 132 GTCAGCGCTGGCAAACTGTTGTTGTGACCAATGGGAAAGCAAGTATAACAAAGCT 191  
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 181 ACAAACTCAATCTTACGAGTGAAGCACTGATTATGAGTATTAAGTCAACAGCAAA 240  
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 252 TGGTGGTGAATGATGGCAAAACCCCTAATGAGTGGAGCGCTGATATTCCTGACG 311  
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 301 GAATTATGAAAATGATGATCGCTAAAGCTGTAGCGTGTGCAAGCATATTGTCACTGAG 360  
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 312 GAATTATGAAAATGATGATCGCTAAAGCTGTAGCGTGTGCAAGCATATTGTCACTGAG 371  
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 361 CAAGGCTTACAGCTGGGCGGATGGAAAAGTCATTGTGAGACCATGACGTCACAGCT 420  
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Db 372 CAAGGCTTACAGCTGGGCGGATGGAAAAGTCATTGTGAGACCATGACGTACAGCT 431  
 QY 421 TACGTTGAGGTTGACCCCTGTAA 444  
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 Db 432 TACGTTGAGGTTGACCCCTGTAA 455  
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 BG937881  
 DEFINITION IABO09006 Bovine Abomasum CDNA Library Bos taurus cDNA 5', mRNA  
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 accession BG937881  
 version BG937881.1 GI:14337253  
 keywords EST.  
 source cow.  
 organism Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 484)  
 Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.  
 CDNA's from bovine abomasum tissue  
 unpublished (2001)  
 contact: Dr. Stephen Moore  
 Beef Genomics Laboratory  
 Dept of AFNS, University of Alberta  
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 Tel: 780 492 0169  
 Fax: 780 492 4265  
 Email: smoores@afns.ualberta.ca  
 The sequence best matches gb:BOVLZYMTA (Bos taurus lysozyme 7A mRNA  
 ) in main database at high score of 959.0 and E-value of 0.0  
 PCR Primers  
 FORWARD: M13 Forward  
 BACKWARD: M13 Reverse  
 Seq primer: T3 primer  
 High quality sequence stop: 484  
 POLYA-No.  
 FEATURES  
 source  
 1..484  
 /location/Qualifiers  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="Bovine Abomasum CDNA Library"  
 /sex="Two males and one female mixed"  
 /tissue\_type="gastrintestinal tissue (GIT)"  
 /cell\_type="Epithelial"  
 /dev\_stage="Young adult"  
 /lab\_host="XLI-BlueMRF"-strain"  
 /note="Organ: Abomasum; Vector: Uni-22APXR; Site\_1: EcoR  
 I; Site\_2: Xho I"  
 BASE COUNT 136 a 97 c 123 g 128 t  
 ORIGIN  
 Query Match 100.0%; Score 444; DB 13; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-223;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ATGAAGGCTCTGCTATTCCTGGGGTTCCTCTTCTGCGCTGCCAAGCAAGTTC 60  
 |||||  
 14 ATGAAGGCTCTGCTATTCCTGGGGTTCCTCTTCTGCGCTGCCAAGCAAGTTC 73  
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 61 TTGAGAGATGTGAGTTGGCTGCAAGTGAAGAACTTGGAGCGCTATTAAGGA 120  
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 74 TTGAGAGATGTGAGTTGGCTGCAAGTGAAGAACTTGGAGCGCTATTAAGGA 133  
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 121 GTCAGCGCTGGCAAACTGTTGTTGTGACCAATGGGAAAGCAAGTATAACAAAGCT 180  
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 134 GTCAGCGCTGGCAAACTGTTGTTGTGACCAATGGGAAAGCAAGTATAACAAAGCT 193  
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 181 ACAAACTCAATCTTACGAGTGAAGCACTGATTATGAGTATTAAGTCAACAGCAAA 240  
 |||||  
 194 ACAAACTCAATCTTACGAGTGAAGCACTGATTATGAGTATTAAGTCAACAGCAAA 253  
 |||||







GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 06:17:08 ; Search time 42 Seconds

(without alignments)  
3242.011 Million cell updates/sec

Title: US-09-978-199-1

Perfect score: 444  
Sequence: 1 atgaagctctcgtattctt.....ttgaggtgtgcacctgtaa 444

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PC1US.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	439	98.9	964	1	US-07-798-223A-1
2	30	6.8	657	4	US-09-385-982-344
3	19	4.3	2044	1	US-08-071-601-3
4	19	4.3	2044	2	US-08-621-100-3
5	18	4.1	20	1	US-08-071-601-15
6	18	4.1	20	2	US-08-621-100-15
7	17	3.8	1120	3	US-08-851-190-4
8	17	3.8	2017	4	US-09-291-922-21
9	16	3.6	43	1	US-08-071-601-11
10	16	3.6	43	2	US-08-621-100-11
11	16	3.6	180	1	US-08-419-078-7
12	16	3.6	180	1	US-08-726-883-7
13	16	3.6	191	1	US-08-419-078-8
14	16	3.6	191	1	US-08-726-883-8
15	16	3.6	206	1	US-08-419-078-12
16	16	3.6	206	1	US-08-726-883-12
17	16	3.6	238	3	US-08-993-254-1
18	16	3.6	300	1	US-08-419-078-4
19	16	3.6	300	1	US-08-726-883-4
20	16	3.6	474	4	US-09-221-017B-429
21	16	3.6	575	4	US-08-858-207A-157
22	16	3.6	1322	1	US-08-419-078-1
23	16	3.6	1322	1	US-08-726-883-1
24	16	3.6	1803	2	US-08-821-119-18
25	16	3.6	1803	2	US-08-821-119-18
26	16	3.6	2760	4	US-09-198-484-1
27	16	3.6	2923	4	US-09-619-353-9

28	16	3.6	4131	1	US-08-309-512-3	Sequence 3, Appl
29	16	3.6	4131	5	PCT-US92-08756A-3	Sequence 3, Appl
30	16	3.6	5077	2	US-08-687-956A-22	Sequence 22, Appl
31	16	3.6	5130	1	US-08-220-401-1	Sequence 1, Appl
32	16	3.6	5130	1	US-08-437-362-1	Sequence 1, Appl
33	16	3.6	5130	1	US-08-437-362-1	Sequence 8, Appl
34	16	3.6	6345	2	US-08-472-809B-8	Sequence 7, Appl
35	16	3.6	38584	4	US-09-453-702B-50	Sequence 50, Appl
36	15	3.4	34	4	US-09-151-189-5	Sequence 5, Appl
37	15	3.4	39	3	US-08-865-960-16	Sequence 16, Appl
38	15	3.4	357	4	US-09-134-001C-2435	Sequence 2435, Ap
39	15	3.4	433	4	US-09-397-787-296	Sequence 296, Ap
40	15	3.4	486	4	US-09-134-001C-1740	Sequence 1740, Ap
41	15	3.4	491	1	US-08-133-711-40	Sequence 40, Appl
42	15	3.4	495	4	US-09-134-001C-2480	Sequence 2480, Ap
43	15	3.4	669	4	US-09-328-111-342	Sequence 342, Ap
44	15	3.4	673	4	US-09-040-984-32	Sequence 32, Appl
45	15	3.4	673	4	US-09-123-912-32	Sequence 32, Appl

## ALIGNMENTS

RESULT 1  
US-07-798-223A-1  
; Sequence 1, Application US/07798223A  
; Patent No. 5422108  
GENERAL INFORMATION:  
APPLICANT: MIKROV, T. Erik  
APPLICANT: FILZMAURICE, Leona Claire  
TITLE OF INVENTION: Protection of Plants Against Pathogens  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/798, 223A  
FILING DATE: 19911125  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/762, 679  
FILING DATE: 19-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 51984  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
FAX: (619)552-0095  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 964 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 25..459  
US-07-798-223A-1  
Query Match 98.9%; Score 439; DB 1; Length 964;  
Best Local Similarity 100.0%; Pred. No. 1; Se-226;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-385-982-344
; Sequence 344, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(657)
; OTHER INFORMATION: n - A,T,C or G
US-09-385-982-344

Query Match          6.8%; Score 30; DB 4; Length 657;
Best Local Similarity 100.0%; Prd. No. 1e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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	Query Match	6.8%;	Score 30;	DB 4;	Length 657;
	Best Local Similarity	100.0%;	Pred. No. 1e-06;		
Matches	30;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
QY	204 AAGCACTGATTATGGATATTTCAGACAA	233                         			
Dd	205 AAGCACTGATTATGGATATTTCAGACAA	234			

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Query Match      4.3%; Score 19; DB 1; Length 2044;
Best Local Similarity 100.0%; Pred. NO. 0.91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      371 CAGCCTGGGTGGCATGGA 389
        |||
Db      2036 CAGCCTGGGTGGCATGGA 2018

RESULT 4
US-08-621-100-3/c
; Sequence 3, Application US/08621100
; Patent No. 5850000
;
; GENERAL INFORMATION:
;
; APPLICANT: BLECK, GREGORY T.
; APPLICANT: BREMEL, ROBERT D.

```

TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE  
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL  
STREET: 100 E. WISCONSIN AVE., SUITE 1100  
CITY: MILWAUKEE  
STATE: WI  
COUNTRY: USA  
ZIP: 53202-4178  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,100  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/071,601  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: F. 3262-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 255-2022  
TELEFAX: (608) 255-2182  
TELEX: 26832 ANDSTARK  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2044 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: signal peptide coding region  
LOCATION: 1943..2043  
FEATURE:  
NAME/KEY: inherited control region for a-lactalbumin  
LOCATION: 1966  
FEATURE:  
NAME/KEY: putative steroid response element  
LOCATION: 1433..1446  
FEATURE:  
NAME/KEY: RNA polymerase binding region  
LOCATION: 1961..1978  
US-08-621-100-3  
Query Match 4.3%; Score 19; DB 2; Length 2044;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 CAGCTGGTGGCATGGA 389  
|||||  
Db 2036 CAGCTGGTGGCATGGA 2018

RESULT 5  
US-08-071-601-15  
Sequence 15, Application US/08071601  
Patent No. 5530177  
GENERAL INFORMATION:  
APPLICANT: BLECK, GREGORY T.  
APPLICANT: BREMEL, ROBERT D.  
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE  
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL  
STREET: 100 E. WISCONSIN AVE., SUITE 1100  
CITY: MILWAUKEE  
STATE: WI  
COUNTRY: USA  
ZIP: 53202-4178  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/071,601  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/744,765  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: F. 3262-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 255-2022  
TELEFAX: (608) 255-2182  
TELEX: 26832 ANDSTARK  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-071-601-15  
Query Match 4.1%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 AGCTGGTGGCATGGA 389  
|||||  
Db 1 AGCTGGTGGCATGGA 18

RESULT 6  
US-08-621-100-15  
Sequence 15, Application US/08621100  
Patent No. 5850000  
GENERAL INFORMATION:  
APPLICANT: BLECK, GREGORY T.  
APPLICANT: BREMEL, ROBERT D.  
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE  
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL  
STREET: 100 E. WISCONSIN AVE., SUITE 1100  
CITY: MILWAUKEE  
STATE: WI  
COUNTRY: USA  
ZIP: 53202-4178  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,100  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/071,601  
FILING DATE:

APPLICATION NUMBER: US/07/744,765  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: F. 3262-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 255-2022  
TELEFAX: (608) 255-2182  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-621-100-15

Query Match 4.1%; Score 18; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 AGCCTGGTGGCATGTGGA 389  
DB 1 AGCCTGGTGGCATGTGGA 18

RESULT 7  
US-08-851-190-4  
Sequence 4, Application US/08851190  
Patent No. 6074843  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goll, Surya K.  
TITLE OF INVENTION: HUMAN TSC-22-LIKE PROTEIN  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,190  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0285 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1120 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: TONSNOT01  
CLONE: 736663

US-08-851-190-4

Query Match 3.8%; Score 17; DB 3; Length 1120;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AACCTGAAGAACTTG 100  
DB 1104 AACCTGAAGAACTTG 1120

RESULT 8  
US-09-291-922-21  
Sequence 21, Application US/09291922  
Patent No. 6383776  
GENERAL INFORMATION:  
APPLICANT: Allen, Steve  
APPLICANT: Hiltz, Bill  
APPLICANT: Kinney, Tony  
APPLICANT: Tingey, Scott  
TITLE OF INVENTION: Plant Sugar Transport Proteins  
FILE REFERENCE: BB-1163  
CURRENT APPLICATION NUMBER: US/09/291,922  
CURRENT FILING DATE: 1999-04-14  
EARLIER APPLICATION NUMBER: 60/083,044  
EARLIER FILING DATE: April 24, 1998  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 21  
LENGTH: 2017  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-291-922-21

Query Match 3.8%; Score 17; DB 4; Length 2017;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CTGTGCTGTCCAGGC 54  
DB 1413 CTGTGCTGTCCAGGC 1429

RESULT 9  
US-08-071-601-11  
Sequence 11, Application US/08071601  
Patent No. 5530177  
GENERAL INFORMATION:  
APPLICANT: BLECK, GREGORY T.  
APPLICANT: BREMEL, ROBERT D.  
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDROS, SCALES, STARR & SAWALL  
STREET: 100 E. WISCONSIN AVE., SUITE 1100  
CITY: MILWAUKEE  
STATE: WI  
COUNTRY: USA  
ZIP: 53202-4178  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/071,601  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/744,765  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: F. 3262-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 255-2022  
TELEFAX: (608) 255-2182  
TELEX: 26832 ANDSTARK  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-071-601-11

Query Match 3.6%; Score 16; DB 1; Length 43;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CCTGGTGCATGGAA 389  
DB 22 CCTGGTGCATGGAA 37

RESULT 10  
US-08-621-100-11  
Sequence 11, Application US/08621100  
Patent No. 365000  
GENERAL INFORMATION:  
APPLICANT: BLECK, GREGORY T.  
APPLICANT: BREMEL, ROBERT D.  
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDRUS, SCALES, STARK & SMALL  
STREET: 100 E. WISCONSIN AVE., SUITE 1100  
CITY: MILWAUKEE  
STATE: WI  
COUNTRY: USA  
ZIP: 53202-4178  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,100  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/071,601  
FILING DATE:  
APPLICATION NUMBER: US/07/744,765  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: F. 3262-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 255-2022  
TELEFAX: (608) 255-2182  
TELEX: 26832 ANDSTARK  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-621-100-11

Query Match 3.6%; Score 16; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CCTGGTGCATGGAA 389  
DB 22 CCTGGTGCATGGAA 37

RESULT 11  
US-08-419-078-7  
Sequence 7, Application US/08419078  
Patent No. 5587306  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
APPLICANT: SEILHAMER, JEFFREY J.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/419,078  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: Human Fetal Endothelial - Stressed  
CLONE: 067172  
US-08-419-078-7

Query Match 3.6%; Score 16; DB 1; Length 180;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGACAAGGCAT 368  
DB 155 TCAGTGACAAGGCAT 170

RESULT 12  
US-08-726-883-7  
Sequence 7, Application US/08726883  
Patent No. 5676946  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
APPLICANT: SEILHAMER, JEFFREY J.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,883  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/419,078  
FILING DATE: 10-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: Human Fetal Endothelial - Stressed  
CLONE: 067172  
US-08-726-883-7

Query Match 3.6%; Score 16; DB 1; Length 180;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGACGACGAT 368  
DB 155 TCAGTGACGACGAT 170

RESULT 13  
US-08-419-078-8  
Sequence 8, Application US/08419078  
Patent No. 5587306  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
APPLICANT: SEILHAMER, JEFFREY J.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/419,078  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954

REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: Human Fetal Endothelial - Stressed  
CLONE: 067990  
US-08-419-078-8

Query Match 3.6%; Score 16; DB 1; Length 191;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGACGACGAT 368  
DB 63 TCAGTGACGACGAT 78

RESULT 14  
US-08-726-883-8  
Sequence 8, Application US/08726883  
Patent No. 5676946  
GENERAL INFORMATION:  
APPLICANT: HAWKINS, PHILLIP R.  
APPLICANT: SEILHAMER, JEFFREY J.  
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,883  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/419,078  
FILING DATE: 10-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF0030 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-855-0572  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: Human Fetal Endothelial - Stressed  
CLONE: 067990  
US-08-726-883-8

Query Match 3.6%; Score 16; DB 1; Length 191;

Best Local Similarity 100.0%; Pred. No. 33;  
Matches 16; Conservative 0; Mismatches

0; Indels 0; Gaps 0;

QY 353 TCAGTGAGCAGGCAT 368  
|||||  
DB 63 TCAGTGAGCAGGCAT 78

## RESULT 15

US-08-419-078-12

; Sequence 12, Application US/08419078

; Patent No. 3587306

; GENERAL INFORMATION:

; APPLICANT: HAWKINS, PHILIP R.

; APPLICANT: SEITAMER, JEFFREY J.

; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3330 HILLVIEW AVENUE

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/419,078

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: LUTHER, BARBARA J.

; REGISTRATION NUMBER: 33954

; REFERENCE/DOCKET NUMBER: PF0030 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-855-0572

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 206 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; LIBRARY: Inflamed Adenoid

; CLONE: 159363

; US-08-419-078-12

## Query Match

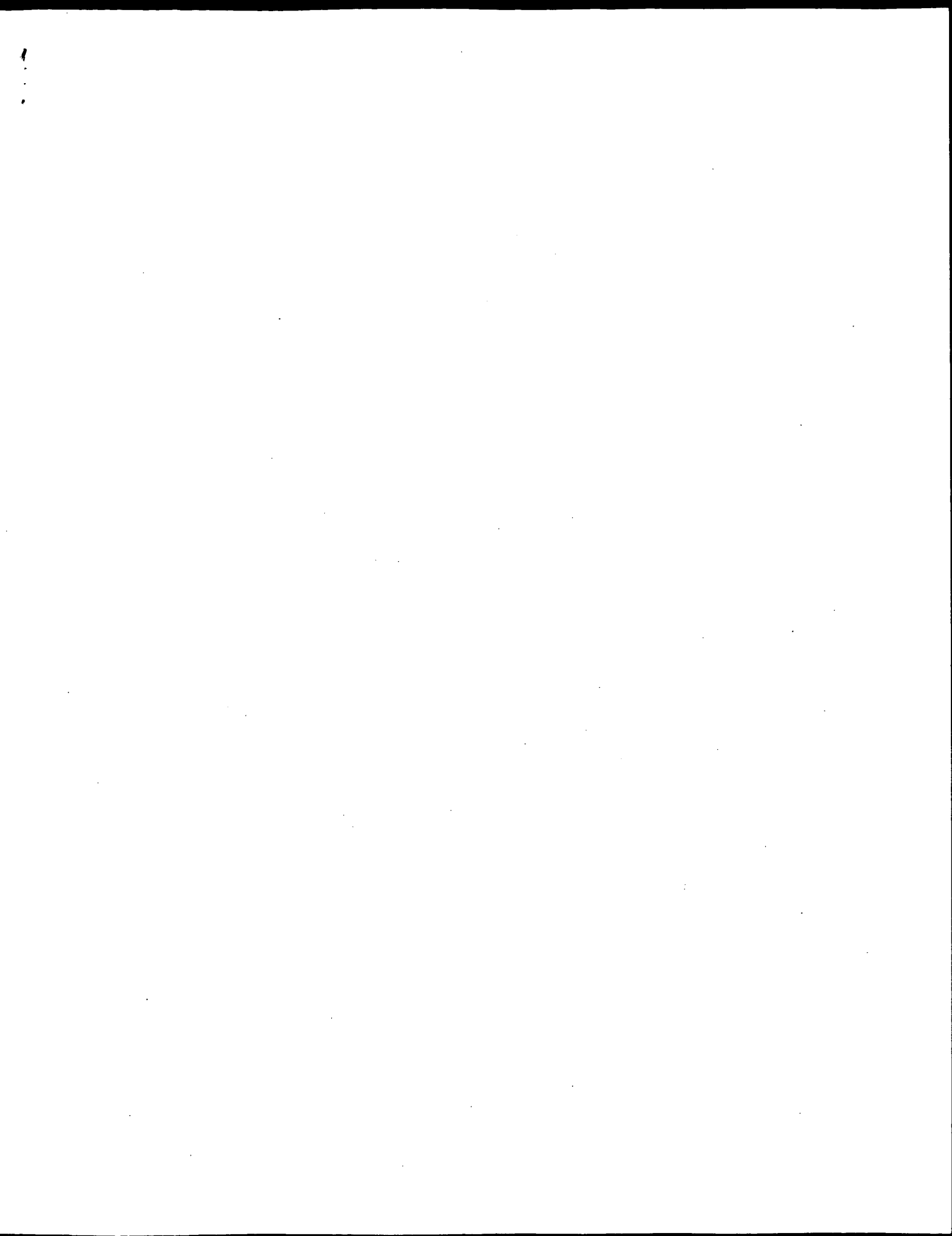
3.6%; Score 16; DB 1; Length 206;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 TCAGTGAGCAGGCAT 368  
|||||  
DB 72 TCAGTGAGCAGGCAT 87

Search completed: July 5, 2003, 07:05:49  
Job time : 43 secs



Result No.	Score	Query Match	Length	DB	ID	Description
1	444	100.0	444	10	US-09-978-199-1	Sequence 1, Appli
2	444	100.0	10132	10	US-09-978-199-3	Sequence 3, Appli
3	30	6.8	367	9	US-09-796-662-8055	Sequence 8055, Ap
4	30	6.8	367	9	US-10-040-862-8055	Sequence 8055, Ap
5	30	6.8	446	9	US-10-066-543-3129	Sequence 3129, Ap
6	30	6.8	478	9	US-10-046-935-1085	Sequence 1085, Ap
7	30	6.8	478	9	US-09-878-178-1085	Sequence 1085, Ap
8	30	6.8	478	9	US-10-146-502-1085	Sequence 1085, Ap
9	30	6.8	522	9	US-10-102-524-791	Sequence 791, App
10	30	6.8	582	9	US-10-046-935-1606	Sequence 1606, Ap
11	30	6.8	582	9	US-09-878-178-1606	Sequence 1606, Ap
12	30	6.8	582	9	US-10-146-502-1606	Sequence 1606, Ap
13	30	6.8	606	9	US-10-060-036-2544	Sequence 2544, Ap
14	30	6.8	636	9	US-09-796-662-8226	Sequence 8226, Ap
15	30	6.8	636	9	US-10-040-862-8226	Sequence 8226, Ap
16	30	6.8	657	9	US-09-871-161-344	Sequence 344, App
17	30	6.8	748	10	US-09-969-347-318	Sequence 318, App
18	30	6.8	2467	10	US-10-001-873-11	Sequence 11, Appl
19	23	5.2	479	9	US-10-025-380-526	Sequence 526, App

C	20	23	5.2	479	10	US-09-922-217-526	Sequence 526, App
C	21	23	5.0	479	10	US-09-833-263-526	Sequence 526, App
C	22	22	5.0	334	9	US-09-771-009-14	Sequence 34, Appl
C	23	22	5.0	233	9	US-10-114-666-117	Sequence 117, App
C	24	22	5.0	233	10	US-09-895-828-117	Sequence 117, App
C	25	20	4.5	1125	9	US-09-815-242-62-6474	Sequence 6474, App
C	26	20	4.5	2612	9	US-10-128-714-158	Sequence 158, App
C	27	20	4.5	3087	9	US-10-128-714-15158	Sequence 5158, App
C	28	19	4.3	30	9	US-09-771-009-15	Sequence 35, Appl
C	29	19	4.3	275	10	US-09-660-352-5019	Sequence 5019, App
C	30	19	4.3	284	10	US-09-660-352-290	Sequence 290, App
C	31	19	4.3	4532	10	US-09-930-377B-1	Sequence 1, Appl1
C	32	19	4.3	55359	10	US-09-804-472-3	Sequence 3, Appl1
C	33	18	4.1	40267	9	US-09-978-244A-25	Sequence 25, Appl1
C	34	17	3.8	425	9	US-09-918-995-36601	Sequence 36601, A
C	35	17	3.8	680	9	US-09-897-511A-3	Sequence 3, Appl1
C	36	17	3.8	680	10	US-09-897-006-3	Sequence 3, Appl1
C	37	17	3.8	724	9	US-10-171-581-244	Sequence 344, App
C	38	17	3.8	2017	9	US-10-051-902-21	Sequence 21, Appl
C	39	17	3.8	2017	9	US-10-051-909-21	Sequence 21, Appl
C	40	17	3.8	2341	9	US-10-037-270-423	Sequence 423, App
C	41	17	3.8	2745	9	US-09-764-891-5859	Sequence 5859, App
C	42	17	3.8	4207	9	US-09-897-511A-4	Sequence 4, Appl1
C	43	17	3.8	4207	10	US-09-897-006-4	Sequence 4, Appl1
C	44	17	3.8	4210	9	US-09-897-511A-5	Sequence 5, Appl1
C	45	17	3.8	4210	10	US-09-897-006-5	Sequence 5, Appl1

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RESULT 1
US-09-978-199-1
Sequence 1, Application US/09978199
Patent No. US20020104126A1
GENERAL INFORMATION:
APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 444
TYPE: DNA
ORGANISM: Bovine sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(441)
US-09-978-199-1

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Query Match	Similarity	100.0%	Score 444;	DB 10;	Length 444;
Best Local	Similarity	100.0%	Pred. No. 1,2e-332;		
Matches 444;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	ATGAAGCCTCTCGTATTCTGTGGGTTTCTCTCTTCTTCTGTGCTGTCCAGGCAAGTTC	60		
	1	ATGAAGGCTCTCTCGTATTCTGTGGGTTTCTCTCTTCTTCTGTGCTGTCCAGGCAAGTTC	60		
Db	61	TTTGAAGATGTGACCTTGCACAACTCTGAAGAACTGTGACTGACGCGCTATTAAGGA	120		
	61	TTTGAAGATGTGACCTTGCACAACTCTGAAGAACTGTGACTGACGCGCTATTAAGGA	120		
QY	121	GTACACCTGTGGCAAACTGTGTGTGTTTGAACCAATGGGAAGCAATTATACAAAGCT	180		
	121	GTACACCTGTGGCAAACTGTGTGTGTTTGAACCAATGGGAAGCAATTATACAAAGCT	180		
Db	181	ACAAACTACAATCTAGCAGTGAAGCACTGATTATGGATATTTTCAGATCAACAGCAA	240		
	181	ACAAACTACAATCTAGCAGTGAAGCACTGATTATGGATATTTTCAGATCAACAGCAA	240		

Db 181 ACAACATACATCTAGACAGTGAAGACATGATTTAGATTTTCAGATCAACAGCAA 240  
QY 241 TGTGTGTATGATGAGAAACCCCTAATGACAGTTACGGCTGCTCATATCTGTGAGC 300  
Db 241 TGTGTGTATGATGAGAAACCCCTAATGACAGTTACGGCTGCTCATATCTGTGAGC 300  
QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTGCAAAAGCATATTTGTCAGTGAG 360  
Db 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTGCAAAAGCATATTTGTCAGTGAG 360  
QY 361 CAAGGCAATACAGCTGGGTGGGATGAGAAAGATGATTTGTGAGACCATGACGTGACAGT 420  
Db 361 CAAGGCAATACAGCTGGGTGGGATGAGAAAGATGATTTGTGAGACCATGACGTGACAGT 420  
QY 421 TACGTTGAGGGTTGACACCTGTAA 444  
Db 421 TACGTTGAGGGTTGACACCTGTAA 444

RESULT 2  
US-09-978-199-3  
; Sequence 3, Application US/09978199  
; Patent No. US20020104126A1  
; GENERAL INFORMATION:  
; APPLICANT: POCHE, GREGORY P.  
; TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS  
; FILE REFERENCE: 42202  
; CURRENT APPLICATION NUMBER: US/09/978,199  
; PRIOR FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: 60/240,967  
; PRIOR FILING DATE: 2000-10-18  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 10132  
; TYPE: DNA  
; ORGANISM: Bovine sp.  
US-09-978-199-3

Query Match 100.0%; Score 444; DB 10; Length 10132;  
Best Local Similarity 100.0%; Pred. No. 1.3e-232;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAAGGCTCTGCTTATTTCTGGGGTTCCTTCCTTTCTGTCGCTGCCAAGCAAGGTC 60  
Db 5767 ATGAAGGCTCTGCTTATTTCTGGGGTTCCTTCCTTTCTGTCGCTGCCAAGCAAGGTC 5826  
QY 61 TTGAGAGATGTGAGCTGCCAGAACTGTGAAGAAACTGTGAGAGCGCTATTAAGGGA 120  
Db 5827 TTGAGAGATGTGAGCTGCCAGAACTGTGAAGAAACTGTGAGAGCGCTATTAAGGGA 5886  
QY 121 GTGAGCTGGCAAACTGTTGTGTTGACCAAAATGGGAAGCAGTTATTAACAAAGCT 180  
Db 5887 GTGAGCTGGCAAACTGTTGTGTTGACCAAAATGGGAAGCAGTTATTAACAAAGCT 5946  
QY 181 ACAAAATTAATCTTACAGTGAAGCACTGATTTATGGGATATTTCAATCAACAGCAA 240  
Db 5947 ACAAAATTAATCTTACAGTGAAGCACTGATTTATGGGATATTTCAATCAACAGCAA 6006  
QY 241 TGTGTGTATGATGAGAAACCCCTAATGACAGTTACGGCTGCTCATATCTGTGAGC 300  
Db 6007 TGTGTGTATGATGAGAAACCCCTAATGACAGTTACGGCTGCTCATATCTGTGAGC 6066  
QY 301 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTGCAAAAGCATATTTGTCAGTGAG 360  
Db 6067 GAATTAATGAAAAATGACATCGCTAAAGCTGTAGCCGTGTGCAAAAGCATATTTGTCAGTGAG 6126  
QY 361 CAAGGCAATACAGCTGGGTGGGATGAGAAAGATGATTTGTGAGACCATGACGTGACAGT 420  
Db 6127 CAAGGCAATACAGCTGGGTGGGATGAGAAAGATGATTTGTGAGACCATGACGTGACAGT 6186  
QY 421 TACGTTGAGGGTTGACACCTGTAA 444

Db 6187 TACGTTGAGGGTTGACACCTGTAA 6210

RESULT 3  
US-09-796-692-8055  
; Sequence 8055, Application US/0996692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Galger, Alexander  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9597  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8055  
; LENGTH: 367  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (331)  
; OTHER INFORMATION: n-A,T,C or G  
; NAME/KEY: unsure  
; LOCATION: (361)  
; OTHER INFORMATION: n-A,T,C or G  
US-09-796-692-8055

Query Match 6.8%; Score 30; DB 9; Length 367;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 204 AAGCAGTATGATGAGATATTTTCAGATCAA 233  
Db 56 AAGCAGTATGATGAGATATTTTCAGATCAA 85  
RESULT 4  
US-10-040-862-8055  
; Sequence 8055, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Galger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Mannion, Jane

```
APPLICANT: Retter, Marc
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8035
LENGTH: 367
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (331)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (361)
OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8035

Query Match 6.8%; Score 30; DB 9; Length 367;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233
DB 56 AAGCACTGATTATGGATATTTTCAGATCAA 85

RESULT 5
US-10-066-543-3129
Sequence 3129, Application US/10066543
Publication No. US20030087818A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Indrias, Carol Joseph
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Carter, Darick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margalita
```

```
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3129
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
US-10-066-543-3129

Query Match 6.8%; Score 30; DB 9; Length 446;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233
DB 4 AAGCACTGATTATGGATATTTTCAGATCAA 33

RESULT 6
US-10-046-935-1085
Sequence 1085, Application US/10046935
Patent No. US20020156011A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1085
LENGTH: 478
TYPE: DNA
ORGANISM: Homo sapiens
US-10-046-935-1085

Query Match 6.8%; Score 30; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCACTGATTATGGATATTTTCAGATCAA 233
DB 189 AAGCACTGATTATGGATATTTTCAGATCAA 218

RESULT 7
US-09-878-178-1085
Sequence 1085, Application US/09878178
Patent No. US20020177552A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1085
LENGTH: 478
TYPE: DNA
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ORGANISM: Homo sapiens  
US-09-878-178-1085

Query Match 6.8%; Score 30; DB 9; Length 478;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233  
DB 189 AAGCAGTATGATGATATTCAGATCAA 218

RESULT 8

US-10-146-502-1085  
Sequence 1085, Application US/10146502  
Publication No. US20030069180A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugui  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Secrist, Heather  
APPLICANT: Wang, Aijun  
APPLICANT: Stolk, John A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.527C2  
CURRENT APPLICATION NUMBER: US/10/146,502  
CURRENT FILING DATE: 2002-05-14  
NUMBER OF SEQ ID NOS: 2241  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1085  
LENGTH: 478  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-146-502-1085

Query Match 6.8%; Score 30; DB 9; Length 478;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233  
DB 189 AAGCAGTATGATGATATTCAGATCAA 218

RESULT 9

US-10-102-524-791  
Sequence 791, Application US/10102524  
Publication No. US20030109434A1  
GENERAL INFORMATION:  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Gaiger, Alexander  
APPLICANT: Gordon, Brian  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER  
FILE REFERENCE: 210121.572  
CURRENT APPLICATION NUMBER: US/10/102,524  
CURRENT FILING DATE: 2002-03-19  
NUMBER OF SEQ ID NOS: 1863  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 791  
LENGTH: 522  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 447, 456, 466  
OTHER INFORMATION: n = A,T,C or G  
US-10-102-524-791

Query Match 6.8%; Score 30; DB 9; Length 522;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233  
DB 56 AAGCAGTATGATGATATTCAGATCAA 85

RESULT 10

US-10-046-935-1606/C  
Sequence 1606, Application US/10046935  
Patent No. US20020136011A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugui  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Secrist, Heather  
APPLICANT: Wang, Aijun  
APPLICANT: Stolk, John A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.527C1  
CURRENT APPLICATION NUMBER: US/10/046,935  
CURRENT FILING DATE: 2002-01-15  
NUMBER OF SEQ ID NOS: 2239  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1606  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-046-935-1606

Query Match 6.8%; Score 30; DB 9; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.7e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233  
DB 511 AAGCAGTATGATGATATTCAGATCAA 482

RESULT 11

US-09-878-178-1606/C  
Sequence 1606, Application US/09878178  
Patent No. US2002017552A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugui  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.527  
CURRENT APPLICATION NUMBER: US/09/878,178  
CURRENT FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 2237  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1606  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-878-178-1606

Query Match 6.8%; Score 30; DB 9; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.7e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AAGCAGTATGATGATATTCAGATCAA 233  
DB 511 AAGCAGTATGATGATATTCAGATCAA 482

RESULT 12

US-10-146-502-1606/C  
Sequence 1606, Application US/10146502  
Publication No. US20030069180A1

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; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1606
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-146-502-1606

Query Match
Best Local Similarity 100.0%; Score 30; DB 9; Length 582;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AACCACTGATTATGGATATTTCAGATCAA 233
Db 511 AACCACTGATTATGGATATTTCAGATCAA 482

RESULT 13
US-10-060-036-2544/c
; Sequence 2544, Application US/10060036
; Publication No. US2003007314A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2544
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 603
; OTHER INFORMATION: n = A,T,C or G
; US-10-060-036-2544

Query Match
Best Local Similarity 100.0%; Score 30; DB 9; Length 606;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AACCACTGATTATGGATATTTCAGATCAA 233
Db 511 AACCACTGATTATGGATATTTCAGATCAA 482

RESULT 14
US-09-796-692-8226
; Sequence 8226, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
```

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8226
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (603)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (615)
; OTHER INFORMATION: n=A,T,C or G
; US-09-796-692-8226

Query Match
Best Local Similarity 100.0%; Score 30; DB 9; Length 636;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 AACCACTGATTATGGATATTTCAGATCAA 233
Db 56 AACCACTGATTATGGATATTTCAGATCAA 85

RESULT 15
US-10-040-862-8226
; Sequence 8226, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and The
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
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DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
PRIORITY FILING DATE: 2000-04-28
PRIORITY APPLICATION NUMBER: US 60/200,779
PRIORITY FILING DATE: 2000-04-28
PRIORITY APPLICATION NUMBER: US 60/200,999
PRIORITY FILING DATE: 2000-05-01
PRIORITY APPLICATION NUMBER: US 60/202,084
PRIORITY FILING DATE: 2000-05-04
PRIORITY APPLICATION NUMBER: US 60/206,201
PRIORITY FILING DATE: 2000-05-22
PRIORITY APPLICATION NUMBER: US 60/218,950
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 60/222,903
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: US 60/223,416
PRIORITY FILING DATE: 2000-08-04
PRIORITY APPLICATION NUMBER: US 60/223,378
PRIORITY FILING DATE: 2000-08-07
PRIORITY APPLICATION NUMBER: US 09/796,592
PRIORITY FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8226
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (603)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (615)
OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8226

Query Match      6.88; Score 30; DB 9; Length 636;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 204 AACGACGATTATGGGATATTTCAGATCAA 233
DB 56 AACGACGATTATGGGATATTTCAGATCAA 85
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